

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 13:01:28 ; Search time 3582 Seconds
(without alignments)
16064.488 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683

Sequence: 1 ttggccactccctctctgcg.....cgcataagaggagtgcccaa 4683

Scoring table: IDENTITY_NUC

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4683	100.0	4683	US-10-696-261-19	Sequence 19, Appli
2	4683	100.0	4683	US-10-696-262-19	Sequence 19, Appli
3	4683	100.0	4683	US-10-696-900-19	Sequence 19, Appli
4	4663.8	99.6	4683	US-10-427-129-6	Sequence 6, Appli
5	4663.8	99.6	4683	US-10-959-017-2	Sequence 2, Appli
6	4663.8	99.6	4683	US-11-145-035-25	Sequence 25, Appli
7	4253.2	90.8	4718	US-10-291-583-6	Sequence 6, Appli
8	4253.2	90.8	4718	US-10-696-261-1	Sequence 1, Appli
9	4253.2	90.8	4718	US-10-696-282-1	Sequence 1, Appli
10	4253.2	90.8	4718	US-10-696-900-1	Sequence 1, Appli
11	4253.2	90.8	4718	US-10-427-129-1	Sequence 1, Appli
12	4253.2	90.8	4718	US-10-959-017-3	Sequence 3, Appli
13	4253.2	90.8	4718	US-11-145-035-19	Sequence 19, Appli
14	3678.4	78.5	4721	US-10-291-583-1	Sequence 1, Appli
15	3678.4	78.5	4721	US-11-145-035-37	Sequence 37, Appli
16	3604.8	77.0	13804	US-10-427-129-11	Sequence 11, Appli
17	3441.6	73.5	4382	US-10-496-799-1	Sequence 1, Appli

18	3404.6	72.7	4385	7	US-10-291-583-5	Sequence 5, Appli
19	3370.4	72.0	4393	7	US-10-291-583-4	Sequence 4, Appli
20	3370.4	72.0	4393	7	US-10-423-704A-1	Sequence 1, Appli
21	3370.4	72.0	4393	15	US-11-145-035-39	Sequence 19, Appli
22	3296.2	70.4	4679	3	US-09-804-898-1	Sequence 1, Appli
23	3296.2	70.4	4679	3	US-09-945-681-10	Sequence 10, Appli
24	3296.2	70.4	4679	6	US-10-038-972A-12	Sequence 12, Appli
25	3296.2	70.4	4679	7	US-10-136-819-6	Sequence 6, Appli
26	3296.2	70.4	4679	15	US-11-145-035-12	Sequence 12, Appli
27	3296.2	70.4	4679	15	US-09-770-315-2	Sequence 2, Appli
28	3293	70.3	4679	15	US-11-184-380-25	Sequence 25, Appli
29	3270.8	69.8	4680	6	US-10-077-294-1	Sequence 1, Appli
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37	3244.2	69.3	4675	3	US-09-782-378A-1	Sequence 1, Appli
38	3244.2	69.3	4675	3	US-09-782-378A-2	Sequence 2, Appli
39	3244.2	69.3	4675	6	US-10-240-198-1	Sequence 1, Appli
40	3244.2	69.3	4675	7	US-10-291-583-7	Sequence 7, Appli
41	3244.2	69.3	4675	8	US-10-427-129-2	Sequence 2, Appli
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44	3182.8	68.0	4722	8	US-10-427-129-3	Sequence 3, Appli
45	3182.8	68.0	4722	15	US-11-145-035-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-10-696-261-19
; Sequence 19, Application US/10696261
; Publication No. US20040057931A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNVN.031USA
; CURRENT APPLICATION NUMBER: US/10/696,261
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
US-10-696-261-19
Query Match 100.0%; Score 4683; DB 8; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TTGGCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGCGCGGACCAAGTGGCC 60
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OY	2401	TCAAAGCGGCGGAATGACAGCGGGCCCTCGAGCAAGCAAGGCGCTAAGACACAGAGGCTCAAA	2460
Db	2401	TCAAAGCGGCGGAATGACAGCGGGCCCTCGAGCAAGCAAGGCGCTAAGACACAGAGGCTCAAA	2460
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Db	2461	CGGGTGAACAATCCGTAACCTGGCGGTATTAACAAGCCGAAGCCGAGTTTCAGGAGCGTCTGC	2520
OY	2521	AAGAAGATAAGCTCTTTTGGGGGCAACCTCGGGCGAGAGTCTTCCAGGCCCAAGAAAGAGG	2580
Db	2521	AAGAAGATAAGCTCTTTTGGGGGCAACCTCGGGCGAGAGTCTTCCAGGCCCAAGAAAGAGG	2580
OY	2581	TTCTCGAATCCTTTTGGTGTGGGTGAGAAAGGTGCTAABAAGGCTCTGGAAGAAAGGTC	2640
Db	2581	TTCTCGAATCCTTTTGGTGTGGGTGAGAAAGGTGCTAABAAGGCTCTGGAAGAAAGGTC	2640
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Db	2641	CGGTAGACAGTCCGCAACAAGAGCCAGACTCCTCCTCGGGCATTTGGCAAGACAGCCAGC	2700
OY	2701	AGCCCGCTAATAAAGAGACTCAATTTTGGTCAAGTGGGACTCAGAGTCAAGTCCCGAAC	2760
Db	2701	AGCCCGCTAATAAAGAGACTCAATTTTGGTCAAGTGGGACTCAGAGTCAAGTCCCGAAC	2760
OY	2761	CACAACTCTGTGGGAAACCTTCAGCAACCCCGCTGTGTGGAGCTTACTATGGCTT	2820
Db	2761	CACAACTCTGTGGGAAACCTTCAGCAACCCCGCTGTGTGGAGCTTACTATGGCTT	2820
OY	2821	CAGCGGTGGCGCAACAATGGCAGACATTAACGAAGGGCGGAGAGTGGGTATAGCT	2880
Db	2821	CAGCGGTGGCGCAACAATGGCAGACATTAACGAAGGGCGGAGAGTGGGTATAGCT	2880
OY	2881	CAGGAATTTGGCATTTGCGATTCCAATGCTGGGCGACAGAGTCATCAACCAAGACC	2940
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Db	2941	GAAATATGGGCTTGTGGCCCACTTATAACAACCACTTCTACAGCAATCTCCAGTGTCTCA	3000
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Db	3001	CGGGGGCCAGCAACGACAAACCACTACTTGGGCTACAGACCCCTGGGGGTATTTGATT	3060
OY	3061	TCAACAGATTCACCTGCCATTCTCACACAGTGACTGGCAGCGACTATCAACAACATT	3120
Db	3061	TCAACAGATTCACCTGCCATTCTCACACAGTGACTGGCAGCGACTATCAACAACATT	3120
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OY	3181	CGAGAAATGATGGCGTCAAGCAACATCGCTAATAACCTTACAGACAGGTTCAAGTCTTGT	3240
Db	3181	CGAGAAATGATGGCGTCAAGCAACATCGCTAATAACCTTACAGACAGGTTCAAGTCTTGT	3240
OY	3241	CGGACTCGGAATACCAATTTCCCGTAAAGTCTCGGCTGCGCACAGAGGCTGCTCCCTC	3300
Db	3241	CGGACTCGGAATACCAATTTCCCGTAAAGTCTCGGCTGCGCACAGAGGCTGCTCCCTC	3300
OY	3301	CGTTCCCGGCGGAAGTGTTCATGATTCGCAAGTACGGGTACTTAACCTCAACATGACA	3360
Db	3301	CGTTCCCGGCGGAAGTGTTCATGATTCGCAAGTACGGGTACTTAACCTCAACATGACA	3360
OY	3361	GCAGAGCGTGGAGCGCTCATCTTTTATCTGCGGAAATATTTCCCATCGGAGATGCTGA	3420
Db	3361	GCAGAGCGTGGAGCGCTCATCTTTTATCTGCGGAAATATTTCCCATCGGAGATGCTGA	3420
OY	3421	GAAAGCGGCAATTAATTTACCTTCAAGCTAACAATTCGAGAGAGTGCCTTTCCACAGCACT	3480

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Db	3541	ACCTGAACAGAACTCAATCATGCTCGGAAGTGCCCAAAACAAGGACTTGTCTTTAGCC	3600
Oy	3601	GTGGGCTTCCAGCTGGCATGTCTGTTCAGCCCAAAAATTGGTACTGGAGCCCTGTAC	3660
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Oy	3661	GGCAGACAGCGGCTTCTTAAACCAAAAACAGACACAAACAGCACTTTACTGGACGTG	3720
Db	3661	GGCAGACAGCGGCTTCTTAAACCAAAAACAGACACAAACAGCACTTTACTGGACGTG	3720
Oy	3721	GTGCTTCAAAATATTAACCTTAATGCGGTGAATCTATATCAACCCTGGCACTGCTATGG	3780
Db	3721	GTGCTTCAAAATATTAACCTTAATGCGGTGAATCTATATCAACCCTGGCACTGCTATGG	3780
Oy	3781	CCTCACACAAAGACGACAAAGCAAGTTCTTTCCATGAGCGGTGTCAATGATTTTGGAA	3840
Db	3781	CCTCACACAAAGACGACAAAGCAAGTTCTTTCCATGAGCGGTGTCAATGATTTTGGAA	3840
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Oy	4321	ATGCAAAATCTGCCAAGCTTGATTTCACTGTGACCAACATGGAATTTATATCTAGCCTC	4380
Db	4321	ATGCAAAATCTGCCAAGCTTGATTTCACTGTGACCAACATGGAATTTATATCTAGCCTC	4380
Oy	4381	GCCCCATTGGACACCCGTTACTCAACCGTCCCTCGTATATTTGTGTGTTATATCAATTAACCG	4440
Db	4381	GCCCCATTGGACACCCGTTACTCAACCGTCCCTCGTATATTTGTGTGTTATATCAATTAACCG	4440
Oy	4441	GTTAATTCGTACAGTTGAACCTTTGGTGTCAATGCTCTTAATATCTTAATCTGTGTCACATA	4500
Db	4441	GTTAATTCGTACAGTTGAACCTTTGGTGTCAATGCTCTTAATATCTTAATCTGTGTCACATA	4500
Oy	4501	GCAACCGGTTACACATTAACCTGTAGTGGCTTCGGAATACCCCTAGTATGATGAGTT	4560
Db	4501	GCAACCGGTTACACATTAACCTGTAGTGGCTTCGGAATACCCCTAGTATGATGAGTT	4560

Dh 4501 GCAACCGGTACACATTAAGTGTGCTTCGGAATACCCCTAAGTAGAGATT 4560
Qy 4561 GCCACCTCCCTTAATGCGCGCTCGCTGCTGGGGCCGCGAGAGAGCTTCGCG 4620
Dh 4561 GCCACCTCCCTTAATGCGCGCTCGCTGCTGGGGCCGCGAGAGAGCTTCGCG 4620
Qy 4621 TCTGCGGACCTTTGGTCCGAGGCGCCACCGAGCGAGCGCGCATAGAGGAGTGGC 4680
Dh 4621 TCTGCGGACCTTTGGTCCGAGGCGCCACCGAGCGAGCGCGCATAGAGGAGTGGC 4680
Qy 4681 CAA 4683
Dh 4681 CAA 4683

RESULT 2
US-10-696-282-19
; Sequence 19, Application US/10696282
; Publication No. US20040057932A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPV.031USA
; CURRENT APPLICATION NUMBER: US/10/696,282
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
US-10-696-282-19

Query Match 100.0%; Score 4683; DB 8; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGGCACTCCCTCTGCGCGCTCGCTCACTAGGCGCGGCGCAAAAGGTGCGC 60
Dh 1 TTGGCACTCCCTCTGCGCGCTCGCTCACTAGGCGCGGCGCAAAAGGTGCGC 60
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Dh 61 CGACGCGCGGCTTTGACCGGGCGGCTCACTAGAGCGAGCGCGCGAGAGGAGTGT 120
Qy 121 GCCAATCTCATCTAGAGGGTCTCTGAGGGGTGAGTCTGACGTGAATTAACGTAG 180
Dh 121 GCCAATCTCATCTAGAGGGTCTCTGAGGGGTGAGTCTGACGTGAATTAACGTAG 180
Qy 121 GGTAGGAGAGTCCGTATTAAGAGTCACTGAGTCTTTCGACATTTTCGACACAT 240
Dh 121 GGTAGGAGAGTCCGTATTAAGAGTCACTGAGTCTTTCGACATTTTCGACACAT 240
Qy 181 GGTAGGAGAGTCCGTATTAAGAGTCACTGAGTCTTTCGACATTTTCGACACAT 240
Dh 181 GGTAGGAGAGTCCGTATTAAGAGTCACTGAGTCTTTCGACATTTTCGACACAT 240
Qy 241 GTGGTCACTGAGTATTAAGCCGAGTGAAGCGAGGCTTCATTTTGAAGCGGGA 300
Dh 241 GTGGTCACTGAGTATTAAGCCGAGTGAAGCGAGGCTTCATTTTGAAGCGGGA 300
Qy 301 GGTGGAACGCGCAGCGCATGCGGGGTTTTCAGATTGTGATTAAGTCCGACGGA 360
Dh 301 GGTGGAACGCGCAGCGCATGCGGGGTTTTCAGATTGTGATTAAGTCCGACGGA 360
Qy 361 CCTTGAAGAGATGCGCGGAGTTCGACAGCTTGTGAACGTGGGCGCGAAGAGA 420
Dh 361 CCTTGAAGAGATGCGCGGAGTTCGACAGCTTGTGAACGTGGGCGCGAAGAGA 420

Qy 421 ATGGAGATGTCGCGCAGATTCGACATGATCTGAATCTGATTTAGAGGACCCCTGAC 480
Dh 421 ATGGAGATGTCGCGCAGATTCGACATGATCTGAATCTGATTTAGAGGACCCCTGAC 480
Qy 481 GGTGGCGGAGAGTGTGAGGCGCATCTTCTGTGTCACTGGCGCGGTGATGTAAGGCCC 540
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Qy 541 GAGAGCCCTCTTCTTGTGATTCGAGAGGAGGAGTCTTACTTCCATCATATTCT 600
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Qy 601 GGTGAGACCAAGGGGTCAAAATTCATGATGTGCGCGCTCTCTGATGATTAAGCA 660
Dh 601 GGTGAGACCAAGGGGTCAAAATTCATGATGTGCGCGCTCTCTGATGATTAAGCA 660
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Qy 721 GACCAAGACGCTAATGCGCGCGGAGGAGAAAGAGTGTGAGAGAGTGTCTACATCC 780
Dh 721 GACCAAGACGCTAATGCGCGCGGAGGAGAAAGAGTGTGAGAGAGTGTCTACATCC 780
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Dh 781 CAATCACTCTCTGCGCAAGACTGAGCCGAGCTGAGTGGGCGTGAATTAAGAGGA 840
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Qy 961 TGTATCCGCTCAAAAACCTCCGACGCTACATGAGCTGTGGGTGAGTGAACG 1020
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Qy 1021 GGGATCACTCTCGAGAGAGAGTGAATCCAGAGAGAACAGGCTCTGATCTCTTCAA 1080
Dh 1021 GGGATCACTCTCGAGAGAGAGTGAATCCAGAGAGAACAGGCTCTGATCTCTTCAA 1080
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Dh 1081 CGCGGCTTCAAATCTCGGAGTCCAGATCAAGGCGCTCTGAGCAATGCGGCAAGATCAT 1140
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Dh 1141 GCGGCTGACCAAAATCCGCGCCGACCTGATAGGCGCGCTCCGCGCGCAATTAA 1200
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Dh 1201 AACCAACCGATTTACCGCATCTCTGAGTGAACGCTAGACCCCTGATACCCGCTC 1260
Qy 1261 CGTCTTCTCGGCTGGGCGGAGAAAGGTTCCGAAAAACGCAACCATCTGGCTGTG 1320
Dh 1261 CGTCTTCTCGGCTGGGCGGAGAAAGGTTCCGAAAAACGCAACCATCTGGCTGTG 1320
Qy 1321 GCGGCGCACAAGGCGCAAGCAATGCGGAAAGCCATGCGCCGCGCTCTTCTA 1380
Dh 1321 GCGGCGCACAAGGCGCAAGCAATGCGGAAAGCCATGCGCCGCGCTCTTCTA 1380
Qy 1381 GCGGTGCTCAATCTGACCAATGAACTTTCCCTTCAAGATTGCGTCAAGAGTGT 1440
Dh 1381 GCGGTGCTCAATCTGACCAATGAACTTTCCCTTCAAGATTGCGTCAAGAGTGT 1440
Qy 1441 GATCTGTGGAAGAGGCAAGATGACGCGCAAGGTGTGAGTGTGCGCAAGGCAATCT 1500
Dh 1441 GATCTGTGGAAGAGGCAAGATGACGCGCAAGGTGTGAGTGTGCGCAAGGCAATCT 1500
Qy 1501 CCGCGGAGCAAGGTGCGCTGAGCAAAAAGTGCAGTCTGCGCCGACATGATCCAC 1560

|||||
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OY 1501
|||||
OY 1551 CCCCGTGTCCGCTCACTCAACACCAACATGTGCCCGGTGATTGACGGGAACAGACAC 1620
Db 1551 CCCCGTGTCCGCTCACTCAACACCAACATGTGCCCGGTGATTGACGGGAACAGACAC 1620
OY 1621 CTTGAGACACGACGAGCGGTTGACGACCGGATGTTCAATTGAACTCAACCGCGCT 1680
Db 1621 CTTGAGACACGACGAGCGGTTGACGACCGGATGTTCAATTGAACTCAACCGCGCT 1680
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Db 1681 GAGAGCATGCTTTGGCAAGTGAACAAGCAGAGATCAAGAGTCTTCCGTGGCGCA 1740
OY 1741 GATATACGTGACCGAGGTGGCGCATGATGTTCTAGTCAAGAAAGGTGAGCCACAACAG 1800
Db 1741 GATATACGTGACCGAGGTGGCGCATGATGTTCTAGTCAAGAAAGGTGAGCCACAACAG 1800
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Db 1801 ACCCGCCCCGATGACGGGATAAAGGAGCCCAAGGGGGCGTGCCTCAGTGGCGGA 1860
OY 1861 TCCATCGACGTTCAGACGGGAAAGAGCTCCGGTGAATCTTGGCCGACAGGTACCAAAACA 1920
Db 1861 TCCATCGACGTTCAGACGGGAAAGAGCTCCGGTGAATCTTGGCCGACAGGTACCAAAACA 1920
OY 1921 ATGTTCTGTGACCGGGGATGCTTCAATGCTGTTTCCCTGCAAAACATGCGAGAGAT 1980
Db 1921 ATGTTCTGTGACCGGGGATGCTTCAATGCTGTTTCCCTGCAAAACATGCGAGAGAT 1980
OY 1981 GAATCAGAAATTTCAACATTTGCTTCAACGCGGACCGAGACGCTTGAGAAATGTTTCC 2040
Db 1981 GAATCAGAAATTTCAACATTTGCTTCAACGCGGACCGAGACGCTTGAGAAATGTTTCC 2040
OY 2041 CGGCGGTGCAGAAATCTCAACCGGTGTCAGAAAGAGAGCTATCCGAAACTGTGCCAT 2100
Db 2041 CGGCGGTGCAGAAATCTCAACCGGTGTCAGAAAGAGAGCTATCCGAGTGTGCCAT 2100
OY 2101 TCATCATCTGCTGGGGGGGGCTCCGAGATGCTTCTGCTGGCTGCGATCTGTCAACGT 2160
Db 2101 TCATCATCTGCTGGGGGGGGCTCCGAGATGCTTCTGCTGGCTGCGATCTGTCAACGT 2160
OY 2161 GGATCTGAGATGACTGTGTTCTGAGCAATAATGACTTAAACAGAGTATGCTGCCAGT 2220
Db 2161 GGATCTGAGATGACTGTGTTCTGAGCAATAATGACTTAAACAGAGTATGCTGCCAGT 2220
OY 2221 GTTATCTTCCAGATTTGCTCGAGAGCAACCTCTCGAGGGCATTCGAGAGTGTGGACT 2280
Db 2221 GTTATCTTCCAGATTTGCTCGAGAGCAACCTCTCGAGGGCATTCGAGAGTGTGGACT 2280
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Db 2281 TGAAAACCTGAGAGCCCGGAAACCAAGCCAAACAGCAAAAGCAGAGCAGCGCGGGT 2340
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Db 2401 TCAACGCGGCGGATGACAGCGGCGCTCGAGCAAGAACAGGCTTACGACAGAGCTCAAG 2460
OY 2461 CGGAGTGAATCCGTAATCTGCGGTAAACACAGCGGAGCTTCAAGAGGCTGTGC 2520
Db 2461 CGGAGTGAATCCGTAATCTGCGGTAAACACAGCGGAGCTTCAAGAGGCTGTGC 2520
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Db 2521 AAGAAGATACGCTTTTGGGGGCAACCTCGGCGAGAGCTTCTCCAGGCAAGAGAGAGG 2580
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Db 2581 TTCTCGAACTTTTGGTCTGTGTTGAGGAAGGTGCTAAGACGGCTCTTGAAGAAACGTC 2640

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Db 3061 TCACAGATTCACATGCAATTTCTACACAGTGACTGGAGCACTCATCAACAACAAT 3120
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Db 3361 GCGAGGCAATGAGAGCTCATCTTTTACCTGCTGGAATTTTCCATCCGAGTGTCTGA 3420
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Db 3421 GAAAGGCAATTAATCTTACCTTACCTGCTGCTACACCTTGAAGAGCTTCCAGAGAGCT 3480
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Db 3481 ACGGCAACAGCAGAGCTGAGCCGCGTGAATTCCTTCATGACCAAGTACTGATAT 3540
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OY 3601 GTGGGTCTCAGAGTGTGCTGTTGAGCCCAAAATGAGCTTCAAGTCTGAGACCTGTTACC 3660
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Db 3661 GGCAGACAGCGGTTTCTAAAAAAGAGCAAGCAACAGCAACCTTACCTGAGCTG 3720

Qy	37121	ATGCTTCAAAATATTAACCTTTAATGGCGGTGAATCTATATACTGAACCTGGCACTGCTAAG	3780
Dp	37121	GTGCTTCAAAATATTAACCTTTAATGGCGGTGAATCTATATACCACTGGCACTGCTAAG	3780
Qy	3781	CCTCACACAAAGACGACAAAGACAAAGTCTTCTTCCATAGCGGTGTCAATGATTTTGGAA	3840
Dp	3781	CCTCACACAAAGACGACAAAGCAAGTCTTCTTCCATAGCGGTGTCAATGATTTTGGAA	3840
Qy	3841	AGGAGAGGCGCGGAGCTTCAAACTGCAATTGGACAAATGTATATGATCAACAGCAAGG	3900
Dp	3841	AGGAGAGGCGCGGAGCTTCAAACTGTCAATTGGACAAATGTATATGATCAACAGCAAGG	3900
Qy	3901	AAATCAAAAGCACTTAAACCCCGTGGCCAACGAAAGATTGGAGACTGTGCACTCATCTCC	3960
Dp	3901	AAATCAAAAGCACTTAAACCCCGTGGCCACGAAAGATTGGAGACTGTGCACTCATCTCC	3960
Qy	3961	AGAGCAGCAGACACAGACCCCTGCGACCGGAGATGTGCAATGTTATGGAGACTTACCTGAA	4020
Dp	3961	AGAGCAGCAGACACAGACCCCTGCGACCGGAGATGTGCAATGTTATGGAGACTTACCTGAA	4020
Qy	4021	TGTGTGTGGCAAGACAGAAAGTATATCTGTGCAAGGTCCTATTTGGGCCAAATTTCTCA	4080
Dp	4021	TGTGTGTGGCAAGACAGAAAGTATATCTGTGCAAGGTCCTATTTGGGCCAAATTTCTCA	4080
Qy	4081	CGGATGAGACATTTTCAACCGGTCTCTCTCATAGGGCGGCTTTGSACTTAAAGCACCGCTC	4140
Dp	4081	CGGATGAGACATTTTCAACCGGTCTCTCTCATAGGGCGGCTTTGSACTTAAAGCACCGCTC	4140
Qy	4141	CTCAGATCTCATCAAAAACAGCGCTGTTCCTGCGAATCTTCGCGAGAGTTTTCGCTA	4200
Dp	4141	CTCAGATCTCATCAAAAACAGCGCTGTTCCTGCGAATCTTCGCGAGAGTTTTCGCTA	4200
Qy	4201	CAAAGTTGCTTCACTTATCAACCAAGTATTCACAGGACAAGTACGCTGAGATGAT	4260
Dp	4201	CAAAGTTGCTTCACTTATCAACCAAGTATTCACAGGACAAGTACGCTGAGATGAT	4260
Qy	4261	GGGAGCTGCAGAAAAGAAAACAGCAAAACGCTGGAATCCGGAAGTCAATATCACTAACT	4320
Dp	4261	GGGAGCTGCAGAAAAGAAAACAGCAAAACGCTGGAATCCGGAAGTCAATATCACTAACT	4320
Qy	4321	ATGCAAAAATTCGCCAACGTTGATTTCACTGTGAGCAACAATGACTTTATATCTAGCCTC	4380
Dp	4321	ATGCAAAAATTCGCCAACGTTGATTTCACTGTGAGCAACAATGACTTTATATCTAGCCTC	4380
Qy	4381	GCCCCATTGGACCCGTTACCTCAACCGGTCCCTGTATTTGTGTATATCAATBAACCG	4440
Dp	4381	GCCCCATTGGACCCGTTACCTCAACCGGTCCCTGTATTTGTGTATATCAATBAACCG	4440
Qy	4441	GTTAATTCGTCAAGTTGAACTTTGCTCATATGTCCTTAATTAATCTTAATCTGATCACA	4500
Dp	4441	GTTAATTCGTCAAGTTGAACTTTGCTCATATGTCCTTAATTAATCTTAATCTGATCACA	4500
Qy	4501	GCAACCGGTTACACTTAACTAGTTGGCTTCGGAATACCCCTAGTAGTAGGATT	4560
Dp	4501	GCAACCGGTTACACTTAACTAGTTAGTGGCTTCGGAATACCCCTAGTAGTAGGATT	4560
Qy	4561	GCCCACTCCCTATAGCGGCTCGTCTGCTGAGTGGGCGCGGCAAGCAGAGACTCTGCG	4620
Dp	4561	GCCCACTCCCTATAGCGGCTCGTCTGCTGAGTGGGCGCGGCAAGCAGAGACTCTGCG	4620
Qy	4621	TCTGCGACCTTTGGTTCGCAAGGCCCAACGACGAGAGCGCATAGAGGAGTGGC	4680
Dp	4621	TCTGCGACCTTTGGTTCGCAAGGCCCAACGAGGAGGAGCGCATAGAGGAGTGGC	4680
Qy	4681	CNA 4683	
Dp	4681	CAA 4683	

RESULT 3
US-10-696-900-19
; Sequence 19, Application US/10696900

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; Publication No. US20040057933A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPV, 031USA
; CURRENT APPLICATION NUMBER: US/10/696,900
; PRIOR APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2003-10-30
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
; US-10-696-900-19

Query Match          100.0%; Score 4683; DB 8; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGCAACCAAGTGC 60
DB      1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGCAACCAAGTGC 60

QY      61 CGAGCGCCGGGCTTTGCCCGGGGGGCTCAGTGAAGCAGAGCGCGCAGAGGGAGTG 120
DB      61 CGAGCGCCGGGCTTTGCCCGGGGGGCTCAGTGAAGCAGAGCGCGCAGAGGGAGTG 120

QY      121 GCCAATCCATCACTAGGGGTTCTGGAGGGGGTGGAGTGTGAAGTGAATTAGTCATAG 180
DB      121 GCCAATCCATCACTAGGGGTTCTGGAGGGGGTGGAGTGTGAAGTGAATTAGTCATAG 180

QY      181 GGTTAGGGAGGTCCTGTATTAGAGGTACAGTGTGTTTGGCACAATTTTGGACACCAT 240
DB      181 GGTTAGGGAGGTCCTGTATTAGAGGTACAGTGTGTTTGGCACAATTTTGGACACCAT 240

QY      241 GTGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGCAGCAGGGTCCCATTTTGAAGCGGGA 300
DB      241 GTGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGCAGCAGGGTCCCATTTTGAAGCGGGA 300

QY      301 GGTTTGAACCGCGACGCGCCANCGCGGGGTTTACGAGATTGTATTAAGGTCCCGACGA 360
DB      301 GGTTTGAACCGCGACGCGCCANCGCGGGGTTTACGAGATTGTATTAAGGTCCCGACGA 360

QY      361 CCTTGAAGACATCTGCCCGGCAATTTTGTGACAGCTTTGTGAACGTGGTGGCCGAGAAAGA 420
DB      361 CCTTGAAGACATCTGCCCGGCAATTTTGTGACAGCTTTGTGAACGTGGTGGCCGAGAAAGA 420

QY      421 ATGGAGATTGGCCGACAGATTCTGACATGATCTGAATCTGATTGAGAGCACCCTCTGAC 480
DB      421 ATGGAGATTGGCCGACAGATTCTGACATGATCTGAATCTGATTGAGAGCACCCTCTGAC 480

QY      481 CGTGGCCGAGAAAGGTGACGGCGCACTTCTGTGTCACTGGCGCGCGTGAAGTAAAGCCCC 540
DB      481 CGTGGCCGAGAAAGGTGACGGCGCACTTCTGTGTCACTGGCGCGCGTGAAGTAAAGCCCC 540

QY      541 GGAGGCGCTCTCTTCTTGTTCAGTTCCGAGAGGGGAGATCTTACTTCCACCTCATATTCT 600
DB      541 GGAGGCGCTCTCTTCTTGTTCAGTTCCGAGAGGGGAGATCTTACTTCCACCTCATATTCT 600

QY      601 GGTGAGACCAACGGGGGTCAAAATCCATGATGTGTGGCCGCTTCTGTGATGATTAAGCA 660
DB      601 GGTGAGACCAACGGGGGTCAAAATCCATGATGTGTGGCGCTTCTGTGATGATTAAGCA 660

QY      661 CAACTGTGTGACACATCTAACCGCGGGATGAGCGCACTGTGCCCACTGTGTTGCGGGT 720
DB      661 CAACTGTGTGACACATCTAACCGCGGGATGAGCGCACTGTGCCCACTGTGTTGCGGGT 720

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Qy 721 GACCAAGACGGTAAATGGGCGGAGGGGGAAACAAGTGTGTGACGATGTCTAATCCC 780
Db 721 GACCAAGACGGTAAATGGGCGGAGGGGGAAACAAGTGTGTGACGATGTCTAATCCC 780
Qy 781 CAACTACCTCTGCGCCCAAGACTCAAGCCGCTGCACTGGGCGTGGAACTTAACATGAGGA 840
Db 781 CAACTACCTCTGCGCCCAAGACTCAAGCCGCTGCACTGGGCGTGGAACTTAACATGAGGA 840
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Db 841 GTATATAAGCGGTGTTTAAACCTTGCGGAGCGCAACGCGCTGTGGCGACGACCTGAC 900
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Db 1201 AACCAACCGCAATTATCCGATCTCTGAGCTGAACGCTTACGACCTTCGCTACGCGGCTC 1260
Qy 1261 CGTCTTTCTCGGCTTGGGCGCAGAAAAGTTGGAAAAAGCAACACATCTGCTTTGG 1320
Db 1261 CGTCTTTCTCGGCTTGGGCGCAGAAAAGTTGGAAAAAGCAACACATCTGCTTTGG 1320
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Qy 1441 GATCTGTGTGGAGAGAGGGCAAGATGAACGCGCAAGTCTGCGTGGAGTCCGCGCAAGGCTTCT 1500
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4683 CAA 4683

RESULT 4
US-10-427-129-6
Sequence 6, Application US/10427129
Publication No. US20040101514A1
GENERAL INFORMATION:
APPLICANT: Liu, Yuhong
APPLICANT: Luo, Jia
TITLE OF INVENTION: High Transgene Expression of A Pseudotyped Adeno-Associated Virus
FILE REFERENCE: 102182-24
CURRENT APPLICATION NUMBER: US/10/427,129
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 09/804,898
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/189,110
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 4683
TYPE: DNA

; ORGANISM: adeno-associated virus 2
US-10-427-129-6

Query Match 99.6%; Score 4663.8; DB 8; Length 4683;
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Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 3961 AGAGCAGACACAGACCTTGGCGAGCGGAGATGTGATTTATGGGAGCTTACCTTGGAA 4020
Db 3961 AGAGCAGACACAGACCTTGGCGAGCGGAGATGTGATTTATGGGAGCTTACCTTGGAA 4020
Qy 4021 TGGTGTGGCAAGACAGAGAGTATACCTGCAAGGCTCTATTTTGGGCAAAATTCCTACA 4080
Db 4021 TGGTGTGGCAAGACAGAGAGTATACCTGCAAGGCTCTATTTTGGGCAAAATTCCTACA 4080
Qy 4081 CGGATGACACTTTCACCCGCTCTCTCTATGGGCGGCTTGTGACTTAAAGCACCCGCTC 4140
Db 4081 CGGATGACACTTTCACCCGCTCTCTCTATGGGCGGCTTGTGACTTAAAGCACCCGCTC 4140
Qy 4141 CTCAAGTCTCATCAAAAAACAAGCTGTCTCTGCAATCTCTCGGCGAGATTTTGGCTA 4200
Db 4141 CTCAAGTCTCATCAAAAAACAAGCTGTCTCTGCAATCTCTCGGCGAGATTTTGGCTA 4200
Qy 4201 CAAAGTTTGTCTTATTCATCAACCAAGTATTCACAAGGACAAGTGAAGTGAAT 4260
Db 4201 CAAAGTTTGTCTTATTCATCAACCAAGTATTCACAAGGACAAGTGAAGTGAAT 4260
Qy 4261 GGGAGCTGCAAAAAGAAAACAGCAAAAGCTGGAATCCGGAAGTGCAGATATCACTTAACT 4320

Db	4261	GGGAGCTGCAAAAAGAAAAACAGCAAACGCTGGAAATCCCGAAGTCAGTAATCATCTAACT	4320
Qy	4321	ATGCAAAATCTGCACACGTTGATTTTCATGTGACAAACAATGSACTTTATCTAGCCTC	4380
Db	4321	ATGCAAAATCTGCCAACGTTGATTTTCATGTGACAAACAATGSACTTTATCTAGCCTC	4380
Qy	4381	GCCCCAATTGCAACCCGTTACCTCACCCGCTCCCTGTAAATTGTGTAAATCAATAAACCG	4440
Db	4381	GCCCCAATTGCAACCCGTTACCTCACCCGCTCCCTGTAAATTGTGTAAATCAATAAACCG	4440
Qy	4441	GTTAATTGTGTCACTGAACTTTGCTCATGTCTTAATTAATCTTAACTGTCAACATA	4500
Db	4441	GTTAATTGTGTCACTGAACTTTGCTCATGTCTTAATTAATCTTAACTGTCAACATA	4500
Qy	4501	GCAACCGGTTACACATTAACTGCTTAAGTGGGCTTGGGAAATACCCCAAGTAAATGSAATT	4560
Db	4501	GCAACCGGTTACACATTAACTGCTTAAGTGGGCTTGGGAAATACCCCAAGTAAATGSAATT	4560
Qy	4561	GCCCACTCTCTATGACGCGCTCGCTCGCTCGGTGGGACCGGACAGAGAGAGACTTGGCG	4620
Db	4561	GCCCACTCTCTATGACGCGCTCGCTCGCTCGGTGGGACCGGACAGAGAGACTTGGCG	4620
Qy	4621	TCTGGAGACTTTGTGTCGCGACAGGCCCAACGAGACAGGACGCGCATAGAGGAGGTGGC	4680
Db	4621	TCTGGAGACTTTGTGTCGCGACAGGCCCAACGAGACAGGACGCGCATAGAGGAGGTGGC	4680
Qy	4681	CAAA 4683	
Db	4681	CAAA 4683	

RESULT 5
US-10-959-017-2

Sequence 2 Application US/10959017
Publication No. US20050106125A1
GENERAL INFORMATION:
APPLICANT: FALCK-PEDERSEN, ERIK S
APPLICANT: PHILPOT, NICOLA
TITLE OF INVENTION: USE OF AA V INTEGRATION EFFICIENCY ELEMENT FOR MEDIATING
TITLE OF INVENTION: SITE-SPECIFIC INTEGRATION OF A TRANSCRIPTION UNIT
FILE REFERENCE: 230526
CURRENT APPLICATION NUMBER: US/10/959, 017
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/US03/11191
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/371,044
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 4683
TYPE: DNA
ORGANISM: adeno-associated virus serotype 6
US-10-959-017-2

Query Match	99.6%	Score 4663.8;	DB 10;	Length 4683;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 4671; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

Qy	1	TTGGCACA	CTCCTCTCTG	CGGCTG	CGCTCA	TGAGCC	GGCGCA	CCAAAG	TCGC	60
		TTGGCACA	CTCCTCTCTG	CGGCTG	CGCTCA	TGAGCC	GGCGCA	CCAAAG	TCGC	60
Db	1	TTGGCACA	CTCCTCTCTG	CGGCTG	CGCTCA	TGAGCC	GGCGCA	CCAAAG	TCGC	60
Qy	61	CGAGGCC	CGGGCTT	GGCCGGG	CGGCTCA	TGAGCG	AGCGCG	GAGAGG	AGTG	120
		CGAGGCC	CGGGCTT	GGCCGGG	CGGCTCA	TGAGCG	AGCGCG	GAGAGG	AGTG	120
Db	61	CGAGGCC	CGGGCTT	GGCCGGG	CGGCTCA	TGAGCG	AGCGCG	GAGAGG	AGTG	120
Qy	121	GCCAACT	CCATC	AC	TGAGGGG	TTCC	TGAGGGG	TGAGCG	GACG	180
		GCCAACT	CCATC	AC	TGAGGGG	TTCC	TGAGGGG	TGAGCG	GACG	180
Db	121	GCCAACT	CCATC	AC	TGAGGGG	TTCC	TGAGGGG	TGAGCG	GACG	180
Qy	181	GGTTAGG	AGGTC	CTGTAT	TGAGAGG	TCAC	TGAGT	TTTTG	CGCAT	240
		GGTTAGG	AGGTC	CTGTAT	TGAGAGG	TCAC	TGAGT	TTTTG	CGCAT	240
Db	181	GGTTAGG	AGGTC	CTGTAT	TGAGAGG	TCAC	TGAGT	TTTTG	CGCAT	240

Db	181	GGTTAGGGAGGCTCTGTATTGAGGTGACGTGAGTGTTTGCGACATTTTGGCACATTTGGACACCAT	240
Qy	241	GGGTGACACGCTGGGTATTTAAGCCCGGATGAGACGACAGGGCTCATTTTGAAGCGGGA	300
Db	241	GTGGTCACGCTGGGTATTTAAGCCCGGATGAGACGACAGGGCTCATTTTGAAGCGGGA	300
Qy	301	GGTTTGAACGGCGACGGCCATGCGGGGTTTTCAGATGTGTGATTAAGTCCCGACGA	360
Db	301	GGTTTGAACGGCGACGGCCATGCGGGGTTTTCAGATGTGTGATTAAGTCCCGACGA	360
Qy	361	CTTTAACGACATCTGCCCCGGCATTTTCTGACAGCTTTGTGAACGTGGGTGGCCGAGAAGA	420
Db	361	CTTTAACGACATCTGCCCCGGCATTTTCTGACAGCTTTGTGAACGTGGGTGGCCGAGAAGA	420
Qy	421	ATGGAGTTGGCCGCGAGATTCTGACATGATCTGAACTTGATTGAGCAGGACCCCTGAC	480
Db	421	ATGGAGTTGGCCGCGAGATTCTGACATGATCTGAACTTGATTGAGCAGGACCCCTGAC	480
Qy	481	CGTGGCCGAGAGCTGCAAGCGGACCTTCCTGGTCCACTGGCGCGCGGTGAGTAAGGCCCC	540
Db	481	CGTGGCCGAGAGCTGCAAGCGGACCTTCCTGGTCCACTGGCGCGCGGTGAGTAAGGCCCC	540
Qy	541	GAGGCGCCCTCTTCTTTGTTCAGTTGAGAGAGGGCGAGTCTTACCTTCATATTTCT	600
Db	541	GAGGCGCCCTCTTCTTTGTTCAGTTGAGAGAGGGCGAGTCTTACCTTCATATTTCT	600
Qy	601	GGTGAGACCAAGGGGGGTCAATCATGATGATGCGGCGCTTCCGATCCAGATTAGGGA	660
Db	601	GGTGAGACCAAGGGGGGTCAATCATGATGATGCGGCGCTTCCGATCCAGATTAGGGA	660
Qy	661	CAAGCTGTGTGAGACCATCTACCGCGGATGAGCGCGACCCCTGCGCACTGGTTGCGCGT	720
Db	661	CAAGCTGTGTGAGACCATCTACCGCGGATGAGCGCGACCCCTGCGCACTGGTTGCGCGT	720
Qy	721	GACCAAGACGCGTAAATGGCGCCGAGAGGGGGAACAAGTGTGACGAGTCTACATCC	780
Db	721	GACCAAGACGCGTAAATGGCGCCGAGAGGGGGAACAAGTGTGACGAGTCTACATCC	780
Qy	781	CAACTACTCTCTCGCCCAAGACTCAAGCCCGGACTGAGTGGCGTGGACTTAATAGAGGA	840
Db	781	CAACTACTCTCTCGCCCAAGACTCAAGCCCGGACTGAGTGGCGTGGACTTAATAGAGGA	840
Qy	841	GTAATTAAAGCGTGTTTAAACTTGGCGGACGCAAAAGGCTGTGGCGCAGCACTTAC	900
Db	841	GTAATTAAAGCGTGTTTAAACTTGGCGGACGCAAAAGGCTGTGGCGCAGCACTTAC	900
Qy	901	CCAGCTCAGCCAGAACCCAGAGCAGAAACAGAGAAATCTGAACCCCAATTCTGACGCGC	960
Db	901	CCAGCTCAGCCAGAACCCAGAGCAGAAACAGAGAAATCTGAACCCCAATTCTGACGCGC	960
Qy	961	TGTATCTCCGGTCAAAAACTCCGCAAGCTAATGGAAGTGGTGGGTGGTGGTGGACCG	1020
Db	961	TGTATCTCCGGTCAAAAACTCCGCAAGCTAATGGAAGTGGTGGGTGGTGGTGGACCG	1020
Qy	1021	GGGCACTACCTCCGAGAAAGAGTGAATCAGAGAGACAGGCTCTGTACATCTCTTCAA	1080
Db	1021	GGGCACTACCTCCGAGAAAGAGTGAATCAGAGAGACAGGCTCTGTACATCTCTTCAA	1080
Qy	1081	CGCGGCTTCAACTCGCGGTCCAGATCAAGGCGCTCTGAGCAATGCGCGCAAGATCAT	1140
Db	1081	CGCGGCTTCAACTCGCGGTCCAGATCAAGGCGCTCTGAGCAATGCGCGCAAGATCAT	1140
Qy	1141	GGCGGTGACCAAAATCCGGCGCCGACTACTCTGTGTAGCCCGCTCCGCGCGCAATTAA	1200
Db	1141	GGCGGTGACCAAAATCCGGCGCCGACTACTCTGTGTAGCCCGCTCCGCGCGCAATTAA	1200
Qy	1201	AACCAACCGCATTTTAACGATCTCGAGAGCTGAACGGGCTACGACCTTGTCTTACGCGGCTC	1260
Db	1201	AACCAACCGCATTTTAACGATCTCGAGAGCTGAACGGGCTACGACCTTGTCTTACGCGGCTC	1260
Qy	1261	CGTCTTCTCGGCTGGGCGCAAAAAGTTTCGAAAAACGCAACAATTGGCTGTTTGG	1320

Dh 1261 GGTCTTCTCGGCTGGGCCAGAAAAGGTTCGAAAAACGCAACACATCTGCTGTTGG 1320
Qy 1321 GCGGCCACCAACCGGCAAGAACCAATCGCGGAAGCCATTCGCCACGCCGCTTCTTA 1380
Dh 1321 GCGGCCACCAACCGGCAAGAACCAATCGCGGAAGCCATTCGCCACGCCGCTTCTTA 1380
Qy 1381 CCGCTGGCTCAACTGAGCAATGAGAACTTTCCCTTCAACGATTGCGTCAAGATAGT 1440
Dh 1381 CCGCTGGCTCAACTGAGCAATGAGAACTTTCCCTTCAACGATTGCGTCAAGATAGT 1440
Qy 1441 GATCTGGTGGAGAGAGGCAAGATGACGGCCAAAGTCGTGAGTCCGCCAAAGCCATTCT 1500
Dh 1441 GATCTGGTGGAGAGAGGCAAGATGACGGCCAAAGTCGTGAGTCCGCCAAAGCCATTCT 1500
Qy 1501 CCGGGGAGCAAGGTGCGCGTGGACCAAAAGTGAAGTCCTCCGCCAGATCCATCCAC 1560
Dh 1501 CCGGGGAGCAAGGTGCGCGTGGACCAAAAGTGAAGTCCTCCGCCAGATCCATCCAC 1560
Qy 1561 CCGCGTATCGTCACTCTCAACACCAACATGTGCGCGTGAATTGAACGAGAACACAC 1620
Dh 1561 CCGCGTATCGTCACTCTCAACACCAACATGTGCGCGTGAATTGAACGAGAACACAC 1620
Qy 1621 CTTGAGACACCAAGACCCGTTGACAGACCGGATGTTCAATTTGAACTCACCCGCTCT 1680
Dh 1621 CTTGAGACACCAAGACCCGTTGACAGACCGGATGTTCAATTTGAACTCACCCGCTCT 1680
Qy 1681 GGAACATGACTTTGGCAAGGTGACAAAGCAGAAGTCAAAAGTCTTCGCTGGGCGCA 1740
Dh 1681 GGAACATGACTTTGGCAAGGTGACAAAGCAGAAGTCAAAAGTCTTCGCTGGGCGCA 1740
Qy 1741 GGATCAGCTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGATGAGCCAAACAG 1800
Dh 1741 GGATCAGCTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGATGAGCCAAACAG 1800
Qy 1801 ACCCGCCCCGATGACCGCGGATTAAGGAGCCAAAGCGGCGCTGCTCTAGTCGGGA 1860
Dh 1801 ACCCGCCCCGATGACCGCGGATTAAGGAGCCAAAGCGGCGCTGCTCTAGTCGGGA 1860
Qy 1861 TCCATCGACGTCAAGCGGGAAGGAGCTCGGTGGACTTTGGCGACAGGTACCAAAACAA 1920
Dh 1861 TCCATCGACGTCAAGCGGGAAGGAGCTCGGTGGACTTTGGCGACAGGTACCAAAACAA 1920
Qy 1921 ATGTTCTGTCACCGCGGCACTGCTTCAGATCTGTTCCCTGCAAAACATCGAGAGAT 1980
Dh 1921 ATGTTCTGTCACCGCGGCACTGCTTCAGATCTGTTCCCTGCAAAACATCGAGAGAT 1980
Qy 1981 GAATCAGATTTCAACATTTGCTTCAACGACCGGACAGAGACTGTTCAAGATGTTCC 2040
Dh 1981 GAATCAGATTTCAACATTTGCTTCAACGACCGGACAGAGACTGTTCAAGATGTTCC 2040
Qy 2041 CCGGCGTGCAGAACTCTCAACCGGTCTGAGAAAGGACGTATGGAAACCTCTGGCAT 2100
Dh 2041 CCGGCGTGCAGAACTCTCAACCGGTCTGAGAAAGGACGTATGGAAACCTCTGGCAT 2100
Qy 2101 TCATCATCTGCTGGGCGCGGCTCCCGAGATTGCTTGCCTGCGCTGCGATCTGGTCAACGT 2160
Dh 2101 TCATCATCTGCTGGGCGCGGCTCCCGAGATTGCTTGCCTGCGCTGCGATCTGGTCAACGT 2160
Qy 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAAACAGGTATGCTCCCGATG 2220
Dh 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAAACAGGTATGCTCCCGATG 2220
Qy 2221 GTTATCTTCAGATTGGCTCGAGGACAACTCTGAGGGGCAATTGCGAGAGTGGGACT 2280
Dh 2221 GTTATCTTCAGATTGGCTCGAGGACAACTCTGAGGGGCAATTGCGAGAGTGGGACT 2280
Qy 2281 TGAACCTGAGCCCGGAAACCAAAAGCCAAACAGCAAAACAGAGACGACGCGGCTC 2340
Dh 2281 TGAACCTGAGCCCGGAAACCAAAAGCCAAACAGCAAAACAGAGACGACGCGGCTC 2340
Qy 2341 TGGTGTCTTCTGCTGCTACAAAGTACTCGGACCTTCAACGACTGCAAAAGGGGAGCCCG 2400
Dh 2341 TGGTGTCTTCTGCTGCTACAAAGTACTCGGACCTTCAACGACTGCAAAAGGGGAGCCCG 2400

Qy 2401 TCAACGCGGGGATGACAGCGGCCCTGAGAGACGACAAAGGCTTACGACACAGCTCAAG 2460
Dh 2401 TCAACGCGGGGATGACAGCGGCCCTGAGAGACGACAAAGGCTTACGACACAGCTCAAG 2460
Qy 2461 CCGGTGACCAATCCGTACTCTGCGGTATTAACACGCGGACGCGCGATTTCAAGAGCTGTC 2520
Dh 2461 CCGGTGACCAATCCGTACTCTGCGGTATTAACACGCGGACGCGCGATTTCAAGAGCTGTC 2520
Qy 2521 AAGAAATACGTCTTTTGGGGGCAACTCGGGGAGAGATCTTTCAGAGCCAAAGAGGG 2580
Dh 2521 AAGAAATACGTCTTTTGGGGGCAACTCGGGGAGAGATCTTTCAGAGCCAAAGAGGG 2580
Qy 2581 TTCTCGAACTTTTGGTCTGTTGAGGAAGTGTAAAGCGGCTCTCGAAAGAAACGTC 2640
Dh 2581 TTCTCGAACTTTTGGTCTGTTGAGGAAGTGTAAAGCGGCTCTCGAAAGAAACGTC 2640
Qy 2641 CCGTAGACAGTGCACAAAGGACCAACTCTCTCGGCAATTGGCAAGACGCGCAGC 2700
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Qy 2701 AGCCCGCTAAAAAGACCTCAATTTTGTGACACTGCGCATCAAGATCACTCCCGAAC 2760
Dh 2701 AGCCCGCTAAAAAGACCTCAATTTTGTGACACTGCGCATCAAGATCACTCCCGAAC 2760
Qy 2761 CACAACCTCTCGAGAACTTCAGCAACCCCGCTGAGGAACTTACAAATGACTT 2820
Dh 2761 CACAACCTCTCGAGAACTTCAGCAACCCCGCTGAGGAACTTACAAATGACTT 2820
Qy 2821 CAGCGGTGGCGACCAATGGCAGACAAATTAAGAAAGCGCGGACGAGTGGTATATGCT 2880
Dh 2821 CAGCGGTGGCGACCAATGGCAGACCAATTAAGAAAGCGCGGACGAGTGGTATATGCT 2880
Qy 2881 CAGGAATTTGGCAATGGGATTTCCACATGGCTGGGCGCAAGAGTATCACACAGACCC 2940
Dh 2881 CAGGAATTTGGCAATGGGATTTCCACATGGCTGGGCGCAAGAGTATCACACAGACCC 2940
Qy 2941 GAACATGGGCTTTGCCACACTATTAACCAACCTCTTCAAGCAAAATCTCAGTCTTCAA 3000
Dh 2941 GAACATGGGCTTTGCCACACTATTAACCAACCTCTTCAAGCAAAATCTCAGTCTTCAA 3000
Qy 3001 CCGGGGCGACCAACGACCAACCACTACTGCGCTPACAGACCCCTCGGGGTATTTGATT 3060
Dh 3001 CCGGGGCGACCAACGACCAACCACTACTGCGCTPACAGACCCCTCGGGGTATTTGATT 3060
Qy 3061 TCAACAAATTTCCACTGGCAATTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3120
Dh 3061 TCAACAAATTTCCACTGGCAATTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3120
Qy 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTTTCAACATTCMAAGTCAAGAGGTCA 3180
Dh 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTTTCAACATTCMAAGTCAAGAGGTCA 3180
Qy 3181 CGAGATTCGAGTCACTGCTCACTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3240
Dh 3181 CGAGATTCGAGTCACTGCTCACTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3240
Qy 3241 CCGACTGGAGTCACTGCTCACTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3300
Dh 3241 CCGACTGGAGTCACTGCTCACTTCTCAACAGTACTGGGCGGACGCTATCAACAAATT 3300
Qy 3301 CGTTCCCGGCGAGTGTGATGATTCGAGTACGCGCTACTTAAACGCTCAACAAATTGCA 3360
Dh 3301 CGTTCCCGGCGAGTGTGATGATTCGAGTACGCGCTACTTAAACGCTCAACAAATTGCA 3360
Qy 3361 GCGAGGAGTGGAGCGCTCATCTTTTACTGCTGGAAATTTTCCATCGCAAGTCTGTA 3420
Dh 3361 GCGAGGAGTGGAGCGCTCATCTTTTACTGCTGGAAATTTTCCATCGCAAGTCTGTA 3420
Qy 3421 GACCGGCAATTAACCTTCAAGTACACCTTTCAGAGAGCGGCTTTCACAGAGCT 3480
Dh 3421 GACCGGCAATTAACCTTCAAGTACACCTTTCAGAGAGCGGCTTTCACAGAGCT 3480

QY 3481 ACGGACAGAGCCAGAGCTGAGCCGGCTGATGATCTCTCATGCAAGCACTGTATTT 3540
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Db 3481 ACGGACAGAGCCAGAGCTGAGCCGGCTGATGATCTCTCATGCAAGCACTGTATTT 3540
QY 3541 ACTGGAACAGAACTTCAGAACTAGTCCGGAAGTCCCAAAACAGAGACTTGTCTTTAGCC 3600
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Db 3541 ACTGGAACAGAACTTCAGAACTAGTCCGGAAGTCCCAAAACAGAGACTTGTCTTTAGCC 3600
QY 3601 GTGGGTCTCCGAGCTGGGCACTGTCTGTTCAGCCCAAAACTGGCTACTGTGACCCCTTTACC 3660
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Db 3601 GTGGGTCTCCGAGCTGGGCACTGTCTGTTCAGCCCAAAACTGGCTACTGTGACCCCTTTACC 3660
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Db 3661 GGCAGACAGCGGCTTCTTAAACAAAACAGACAAACAGCACTTTACTGTGACCTG 3720
QY 3721 GTGCTTCAAAATATATACCTTATATGGGCGTGAATCTATATCAACCTGCACTGTATGG 3780
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Db 3721 GTGCTTCAAAATATATACCTTATATGGGCGTGAATCTATATCAACCTGCACTGTATGG 3780
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Db 3961 AGACACAGAGACAGACCCCTGCGACCGGAGATGTCAGATGTTATGGAGCTTACTGTGAA 4020
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QY 4141 CTCGATTCCTATCAAAAACAGCGCTGTCTCTGGAATCTCTCCGACAGATTTTGGGCTTA 4200
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QY 4201 CAAAGTTTGTCTCATCTTCAATCCAGTATTCACAGGACAAAGTGGAGGCTGGAGATTGAAT 4260
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Db 4201 CAAAGTTTGTCTCATCTTCAATCCAGTATTCACAGGACAAAGTGGAGGCTGGAGATTGAAT 4260
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Db 4261 GGGAGCTGACAGAAAGAAACAGCAACGCTGGAATCCGGAAGTGCAGATATCATCTAACT 4320
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Db 4381 GCCCATTTGGGACCCGTTACTCAACCGTCCCTGTATATTTGTGTTATATATTAACCG 4440
QY 4441 GTTAATTCGTCTCAGTTGAATTTGTCTCATGTCTTATATCTTATCTGTGACCAATA 4500
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Db 4441 GTTAATTCGTCTCAGTTGAATTTGTCTCATGTCTTATATCTTATCTGTGACCAATA 4500
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Db 4561 GCCCACTCCCTTATATGCGCGCTCGCTCGTGGTGGGCGCGGACAGAGCAAGCTCTGCGG 4620
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QY 4681 CAA 4683
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Db 4681 CAA 4683
| | | | |
RESULT 6
US-11-145-035-25
; Sequence 25, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: MAV VECTORS AND METHODS
; FILE REFERENCE: 28335/4135
; CURRENT APPLICATION NUMBER: US/11/145,035
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 25
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: Adeno-associate virus 6
US-11-145-035-25
Query Match 99.6%; Score 4663.8; DB 15; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 TTGGCACTCCCTTCTTGGCGGCTGCTCGCTCATGAGCGCGGCGCAACCAAGTGGCC 60
| | | | |
Db 1 TTGGCACTCCCTTCTTGGCGGCTGCTCGCTCATGAGCGCGGCGCAACCAAGTGGCC 60
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QY 61 CGAGCGCGGCGCTTGGCGGCGGCGCTCAAGTGAAGGAGGCGGAGGAGGAGTGG 120
| | | | |
Db 61 CGAGCGCGGCGCTTGGCGGCGGCGCTCAAGTGAAGGAGGAGGAGGAGGAGTGG 120
| | | | |
QY 121 GCCAATTCATCACTAAGGAGTCTGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
| | | | |
Db 121 GCCAATTCATCACTAAGGAGTCTGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
| | | | |
QY 181 GGTGAGGAGGCTCTGATTAAGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
| | | | |
Db 181 GGTGAGGAGGCTCTGATTAAGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
| | | | |
QY 241 GTGCTACGCTGGGTATTTAAGCCCGAGTGAAGCAAGGAGTCCCAATTTGAAGCGGGA 300
| | | | |
Db 241 GTGCTACGCTGGGTATTTAAGCCCGAGTGAAGCAAGGAGTCCCAATTTGAAGCGGGA 300
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QY 301 GGTGGAACGCGAGCGCCATAGCGGAGTTTACGAGATTTGAAGTGAAGTGAAGTGAAG 360
| | | | |
Db 301 GGTGGAACGCGAGCGCCATAGCGGAGTTTACGAGATTTGAAGTGAAGTGAAGTGAAG 360
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QY 361 CTTTGAAGAGATTCGCGCGGCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
| | | | |
Db 361 CTTTGAAGAGATTCGCGCGGCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
| | | | |
QY 421 ATGGGAGTTGCGCGCAGATTTCTGACATGATGTAATCTGATTTGAGCAGGACCCCTGAC 480
| | | | |
Db 421 ATGGGAGTTGCGCGCAGATTTCTGACATGATGTAATCTGATTTGAGCAGGACCCCTGAC 480
| | | | |
QY 481 CGTGGCGAAGAGCTGAGCGGCACTTCTGTGTCATGCGCGCGCTGAGTGAAGGCCCC 540
| | | | |
Db 481 CGTGGCGAAGAGCTGAGCGGCACTTCTGTGTCATGCGCGCGCTGAGTGAAGGCCCC 540
| | | | |

Qy 541 GGAGCCCTCTTCTTGTGAGTTGAGAGGAGGAGGCTTACTTCCACTTCATTTCT 600
Db 541 GGAGCCCTCTTCTTGTGAGTTGAGAGGAGGAGGCTTACTTCCACTTCATTTCT 600
Qy 601 GGTGAGAGCCA GGGGGGTCAAAATCCATGCTGCGGCGCTTCTGAGTCAGATTAGGA 660
Db 601 GGTGAGAGCCA GGGGGGTCAAAATCCATGCTGCGGCGCTTCTGAGTCAGATTAGGA 660
Qy 661 CAACCTGCTGAGACCATCTACCGCGGATGAGACCCGACCTTGGCCCAATGCTTCCGCGT 720
Db 661 CAACCTGCTGAGACCATCTACCGCGGATGAGACCCGACCTTGGCCCAATGCTTCCGCGT 720
Qy 721 GACCAAGACGCTATGAGCGCGGAGGGGGAGCAAGGTGCTGAGACGATCTCATCTCC 780
Db 721 GACCAAGACGCTATGAGCGCGGAGGGGGAGCAAGGTGCTGAGACGATCTCATCTCC 780
Qy 781 CAACCTACTCTGCTCCAAAGACTAGCCCGAGCTGCACTGCGGCTGAGCTTAACTAGAGGA 840
Db 781 CAACCTACTCTGCTCCAAAGACTAGCCCGAGCTGCACTGCGGCTGAGCTTAACTAGAGGA 840
Qy 841 GTATATAAGCGCGTGTTTAACTTGGCCGAGCGCAAAAGGCTGCGGCAAGACTGAC 900
Db 841 GTATATAAGCGCGTGTTTAACTTGGCCGAGCGCAAAAGGCTGCGGCAAGACTGAC 900
Qy 901 CCAGCTCAGCAGACCCAGAGAGAGAA CAAGAGATCTGAACCCCAATTTCTGACGCGCC 960
Db 901 CCAGCTCAGCAGACCCAGAGAGAGAA CAAGAGATCTGAACCCCAATTTCTGACGCGCC 960
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Db 961 TGTCACTCGGTCAAAAACCTTCGCA CGCTATCATGAGCTGCTGCGGTGCTGAGACG 1020
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Db 1381 CGGCTGCTCAACTGGAACCAATGGAATTTCCTTCAAGATTGCGTGCAGAGATGCT 1440
Qy 1441 GATCTGCTGAGAGAGGCGCAAGATGACGCGCAAGGTCGTGAGTCCGCGCAAGGCAATCT 1500
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Db 1921 ATGTTCTGTCACGCGGGCATGCTTCAGATGCTGTTCCCTGCAAAAATGCGAGAAAT 1980
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Qy 3481 ACGGCGACAGCCAGAGCTTGAAGCTGAGTGAATCTCTCATCAAGCAATCTGTAT 3540
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Qy 3841 AGGAGAGCGCGGAGCTTCAACACACTGATTTGGACAAATGTATATTCACAGAGAGG 3900
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Qy 4441 GTTAATTCGAGTGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4500
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Qy 4561 GCCCACTTCTCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620
Db 4561 GCCCACTTCTCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620
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Qy 4681 CAA 4683
Db 4681 CAA 4683

RESULT 7
US-10-291-583-6
; Sequence 6, Application US/10291583
; Publication No. US20030138772A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; APPLICANT: Alviria, Mauricio
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (AAV) Sequences and Isolating No. US20030138772A1 Sequences Identifi

FILE REFERENCE: UPN-02735USA
CURRENT APPLICATION NUMBER: US/10/291,583
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/350,607
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/341,117
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/377,066
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 60/386,675
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 4718
TYPE: DNA
ORGANISM: adeno-associated virus serotype 1
US-10-291-583-6

Query Match 90.8%; Score 4253.2; DB 7; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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DB 121 GGCAATCTCATCTAGAGGTATCGGGAAGCGCTCCACGCTGCCCGCTCAACGCTGA 180
QY 164 CGTGAATTCGTATAGGAGGTTAGGAGGTCCTGTATTAAGAGTCACTGAGTG--TTTTGC 222
DB 181 CGTAAATTAAGTATAGG---GAGTGGTCTGTATTAAGTGTCAACGTGAGTGTTCG 237
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DB 238 GACATTTTGGCAACCATGTGTCAACGCTGGGTATTTAAGCCGAGTGAAGACAGAGAT 297
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QY 343 GATTAAAGTCCCCAGCGACTTTGACGAGCATCTGCCGCAATTTCTGACAGCTTTGTGA 402
DB 358 GATCAAGGTGCGGAGCGACTGACGAGCACTGCGCGGGCAATTTCTGACTGTTGTGAG 417
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QY 463 TGAACAGGCAACCTCTGACCTGTGCGGAGAACTGACGCGCACTTCTGTCCACTGCGG 522
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DB 718 GCCCACTGTTCCGGGTGACCAAGACCGTAAATGCGCGGAGGGGGAACAAAGTGT 777
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DB 838 GTGACTTAACATGAGAGGATATTAAGCGGCTTTTAAACTGCGCGAGCGCAACGCGCT 897
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1903 CGACAGGATACCAAAACAATGTTCTCTGTCACGCGGGACATGCTTCAGATGCTGTTCCCTG 1962
1918 CGACAGGATACCAAAACAATGTTCTCTGTCACGCGGGACATGCTTCAGATGCTGTTCCCTG 1977
1963 CAAAACATGCCAGAGAGATGAATCAGAAATTTCAACATTTGCTTCACGCAACGGGACCAAGAGA 2022
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2323 AGAAGACGCGCGGGGCTTGTGCTTCTGTGCTCAAGTACCTCGAACCTTTCAACGAGC 2382
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2758 CAGAGTCAAGTCCCGGATCCCAACCTCTCGGAGAAACCTCCGAGCAACCCCGCTGCTG 2817
2803 GACCTACTACAATGCTTCAAGCGGTGCGACCAATGCGACAAATTAACGAGAGCGCG 2862
2818 GACCTACTACAATGCTTCAAGCGGTGCGACCAATGCGACAAATTAACGAGAGCGCG 2877
2863 ACGAGTGGGTAATGCTTCAAGAAATTTGCAATTTGCAATGCTGCGGCGACAGAG 2922
2878 ACGAGTGGGTAATGCTTCAAGAAATTTGCAATTTGCAATGCTGCGGCGACAGAG 2937

2923 TCATCACCAACGAGCAGCCGGAATATGAGGCTTGGCCACCTATTAACACCACTCTTACAGAGC 2982
2938 TCATCACCAACGAGCAGCCGGAATATGAGGCTTGGCCACCTATTAACACCACTCTTACAGAGC 2997
2983 AAATCTCCAGTCTTCAACGCGGGGCGACGAAACGACAACTACTTTCGGCTACAGACACC 3042
2998 AAATCTCCAGTCTTCAACGCGGGGCGACGAAACGACAACTACTTTCGGCTACAGACACC 3057
3043 CCTGGGGATATTTGATTTCAACAGATTCCTGCGATTTCTACACAGTGAATGCGAGC 3102
3058 CCTGGGGATATTTGATTTCAACAGATTCCTGCGATTTCTACACAGTGAATGCGAGC 3117
3103 GACTCATCAACAATTTGGGGAATTCGGGCCAAGAGCTCAACTTCAAGGCTCTTCAACA 3162
3118 GACTCATCAACAATTTGGGGAATTCGGGCCAAGAGCTCAACTTCAAGGCTCTTCAACA 3177
3163 TCCAAATCAAGAGATCAACGAGATGAGCTGTCAGACCAATCGCTAATACTTACCA 3222
3178 TCCAAATCAAGAGATCAACGAGATGAGCTGTCAGACCAATCGCTAATACTTACCA 3237
3223 GCACGCTTCAAGTCTTGTTCGAGCTCGAGATCAAGTTCCTGACTCTCGGCTCTGCGC 3282
3238 GCACGCTTCAAGTCTTGTTCGAGCTCGAGATCAAGTTCCTGACTCTCGGCTCTGCGC 3297
3283 ACAGGGGCTGCTCCCTCCGTTCCGGGCGAGCGTTCATGATTCGGCAGTAACGGCTAC 3342
3298 ACAGGGGCTGCTCCCTCCGTTCCGGGCGAGCGTTCATGATTCGGCAGTAACGGCTAC 3357
3343 TAAAGCTCAACAATGAGGAGCGAGCAGTGGAGCTCATCTTTTACTGCTCGAATATT 3402
3358 TGAAGCTCAACAATGAGGAGCGAGCAGTGGAGCTCATCTTTTACTGCTCGAATATT 3417
3403 TCCCATGCGAGATGCTGAGAACGGGCAATTAATTTACTTACGCTACACTTTCAGAGAGC 3462
3418 TCCCTTTCAGATCTGAGAACGGGCAATTAATTTACTTACGCTACACTTTCAGAGAGC 3477
3463 TGCCCTTTCAGAGATGCTGAGAACGGGCAATTAATTTACTTACGCTACACTTTCAGAGAGC 3522
3478 TGCCCTTTCAGAGATGCTGAGAACGGGCAATTAATTTACTTACGCTACACTTTCAGAGAGC 3537
3523 TCGACAGTACCTGATTTACTCTGAAACGAACTCAATCACTGCGGAAGTCCGCAAAACA 3582
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3583 AGGACTGCTGTTTAAAGCGGTGCTTCAGTGCAGTCTGTTTCAAGCCCAAAACTGGGC 3642
3598 AGGACTGCTGTTTAAAGCGGTGCTTCAGTGCAGTCTGTTTCAAGCCCAAAACTGGGC 3657
3643 TACCTGAGACCTGTTTACCGGAGAGAGCGCTTCTAAACGAAACGACAAACAACA 3702
3658 TACCTGAGACCTGTTTATCGGAGAGAGCGCTTCTAAACGAAACGACAAACAACA 3717
3703 GCAACTTACTGAGTGTGCTTCAAAATTAATCTTAAATGAGCGCTGAATCTAATTAACA 3762
3718 GCAATTTACTGAGTGTGCTTCAAAATTAATCTTAAATGAGCGCTGAATCTAATTAACA 3777
3763 ACCCTGCACTGCTATGAGCTTCAACAAGAGCAAGCAATGTTCTTTCCATGAGCG 3822
3778 ACCCTGCACTGCTATGAGCTTCAACAAGAGCAAGCAATGTTCTTTCCATGAGCG 3837
3823 GTGTCATGATTTTGGAAAGAGAGCGCCGAGCTTCAAAACATGCAATGGAACAATGCA 3882
3838 GTGTCATGATTTTGGAAAGAGAGCGCCGAGCTTCAAAACATGCAATGGAACAATGCA 3897
3883 TGATCACAGACGAGAGAAATCAAAAGCACTAACCCCGTGGCCACCGAAGATTTGGGA 3942
3898 TGATCACAGACGAGAGAAATTAAGCACTAACCCCGTGGCCACCGAAGATTTGGGA 3957
3943 CTGTGCAATCAATCTTCAAGAGCAGACAGACCTTGGGACCGGAGATGTGATTTA 4002
3958 CCGTGGCAATCAATTTTCAAGAGCAGACAGACCTTGGGACCGGAGATGTGATTTA 4017
4003 TGGAGGCTTACTGGAATGTGTGCAAGACGATATACCTGCAAGGCTCTAATTT 4062

Db	4018	TGGAGACATTA	CC	TGGCATG	GTGTGGCAAGATAGAGACGTAC	CTGCAGAGGTC	CCATTT	4077
Qy	4063	GGGCCAAATTC	CT	CA	CCGAGTGA	CACTTTCACCCGTCCTCTTCATG	GGGCGGCTTTG	4122
Db	4078	GGGCCAAATTC	CT	CA	CACAGATG	GAACATTTTCCACCGTCCTCTTATG	GGGCGGCTTTG	4137
Qy	4123	GACCTAAGAC	CC	GGCCTCC	TACAGTACCTCAT	TCATCAAAAAACAGCCGTTTCCMGGAATCC	4182	
Db	4138	GACTCAAGAAC	CC	GGCCTCT	CTCAGATCTCAT	CAAAAAACAGCCGTTTCTTGCAATCTC	4197	
Qy	4183	CGGCAAGATTT	CG	GT	CTACAAAGTTTGCTT	CATTCATCACCAAGTATTCACAGACAAG	4242	
Db	4198	CGGCGGAGTTT	CG	GT	CTACAAAGTTTGCTT	CATTCATCACCAATATCTCACAGACAAG	4257	
Qy	4243	TGACCGTGA	GAT	TGAATGG	AGCTGCAAGAAAGAAAACACAAACGCTGGAAATCCGGAAG	4302		
Db	4258	TGAATGGA	AAAT	TGAATGG	AGCTGCAAGAAAGAAAACACAAACGCTGGAAATCCGGAAG	4317		
Qy	4303	TGCAGTATAC	AT	CTA	CTATGCAAAATCTGCAACGTGATTTCACTGTGACAACAATG	4362		
Db	4318	TGCAGTACAC	AT	CTA	CTATGCAAAATCTGCAACGTGATTTCACTGTGACAACAATG	4377		
Qy	4363	GACCTTAT	ACT	AGCCTTC	GGCCCAATG	GCACCCGTTACCTCACCCGTCCTGTAAATGT	4422	
Db	4378	GACCTTAT	ACT	AGCCTTC	GGCCCAATG	GCACCCGTTACCTCACCCGTCCTGTAAATAC	4437	
Qy	4423	GTGTTAAT	CA	ATTAAC	CGGTTAATTCGATCAGTGAACCTTGGTCCATGCTTAATTA	4482		
Db	4438	GTGTTAAT	CA	ATTAAC	CGGTTAATTCGTTCAAGTTGAACCTTGGTCTCCTGCTTCTTA	4497		
Qy	4483	TCTTATCT	GT	GTACCAT	AGCAACCGGTTTACACATTAAC	TCTTAGTTGGCTTGGCGA--	4540	
Db	4498	TCTTATC	-GG	TTAC	CAATGTTATATGCTTACATTAAC	TCTTGGTTGGCCTTGGCAATA	4556	
Qy	4541	-----	-----	-----	-----	-----	4581	
Db	4557	AAAGACTTA	CG	TCAT	CGGGTTTACCCCTAAGATGAAATTTCCCACTCCCTCTGCGCGC	4616		
Qy	4582	TGCGTCGCT	CG	GTGGGGCC	GGCAGAGACAGACTCTGCGCTGCGGAC	CTTTGGTCCGCA	4641	
Db	4617	TGCGTCGCT	CG	GTGGGGCC	CTGGGACCAAGAGTCCGAGACGGCAGAGCTCTGCTGCGC	4676		
Qy	4642	GGCCCA	CCG	AGCGAGCGAGCGCCAT	AGAGGGAGTGGCCAA	4683		
Db	4677	GGCCCA	CCG	AGCGAGCGAGCGCCAGAGGGAGTGGCCAA	4718			
RESULT 8								
US-10-696-261-1								
: Sequence 1, Application US/10696261								
: Publication No. US20040057931A1								
: GENERAL INFORMATION:								
: APPLICANT: Wilson, James M.								
: TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,								
: TITLE OF INVENTION: Vectors and Host Cells Containing Same								
: FILE REFERENCE: GANVPN.031USA								
: CURRENT FILING DATE: US/10/696, 261								
: PRIOR APPLICATION NUMBER: 2003-10-29								
: PRIOR FILING DATE: 2002-02-21								
: PRIOR APPLICATION NUMBER: US 60/107, 114								
: PRIOR FILING DATE: 1998-11-05								
: PRIOR APPLICATION NUMBER: PCT/US99/25694								
: PRIOR FILING DATE: 1999-11-02								
: NUMBER OF SEQ ID NOS: 20								
: SOFTWARE: PatentIn version 3.1								
: SEQ ID NO 1								
: LENGTH: 4718								
: TYPE: DNA								
: ORGANISM: AAV-1								
: FEATURE:								

Query Match	90.8%	Score 4253.2	DB 8	Length 4718
Best Local Similarity	94.7%	Pred. No. 0		
Matches 4471	Conservative	0	Mismatches 208	Indels 43
			Gaps	5
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DB	1	TTGGCCACTCCCTCTCTCTGCGGGCTCGCTCGCTCGGTGGGGCTCGGACCAAAAGTCCGC	60	
QY	61	CGAGCGCCGGGCTTTGCCCGGCGCGCTCACTGAGCGAGCGAGCGAGAGGAGTGT	120	
DB	61	AGACGGGAGAGCTGCTCTGCGCGGCGCGCGAGCGAGCGAGCGAGAGGAGTGT	120	
QY	121	GCCAACTCTCATCACTAGGGGT-----TCTGAGGGGTGAGTCTGTA	163	
DB	121	GCGAACTCTCATCACTAGGGGTATTCGAGAGCGCTCCACGCTGCGCGTCAAGGCTGA	180	
QY	164	CGTGAATTACGCTAAGAGGTTAAGGAGGCTCTGTAATTAGAGTCACTGAGTGT-TTTTGC	222	
DB	181	CGTAAATTACGCTAATGAGG---GAGTGTCTCTGTAATTAGAGTCACTGAGTGTCTTTTC	237	
QY	223	GACATTTTGCAGACACCATGTGTCACTGCTGGTATTTAAGCCCGAGTACGAGAGGT	282	
DB	238	GACATTTTGCAGACACCATGTGTCACTTTAGGGTATATGTGCGAGTACGAGAGAGAT	297	
QY	283	CTCCATTTTGAAGCGGAGGTTTGAACCGCGAGCGCCATGCGGGGTTTACGAGATTGT	342	
DB	298	CTCCATTTTGAAGCGGAGGTTTGAACCGAGACACCATGCGGGCTTCTACGAGATTGT	357	
QY	343	GATTAAAGGTCCCGAGCGACTTGAACGAGCATCTGCGCGGCAATTTTGAACGCTTGTGAA	402	
DB	358	GATCAAGGTGCGGAGCGACTTGAACGAGCATCTGCGGGCAATTTTGAACGCTTGTGTAG	417	
QY	403	CTGGGTGCGAGAGAGGATGGAGTTGCGCGAGATTCTGACATGATCTGAATCTGAT	462	
DB	418	CTGGGTGCGAGAGAGGATGGAGCTCCCGGATTTCTGACATGATCTGAATCTGAT	477	
QY	463	TGAGCAGGCAACCCGAGCGGTGCGGAGAGAGTGTGAGGCGCATCTCGTGTCACTGGG	522	
DB	478	TGAGCAGGCAACCCGAGCGGTGCGGAGAGAGTGTGAGGCGCATCTCGTGTCAATGGG	537	
QY	523	CCGCGTGAAGAGCGCGGAGCGCTTCTTTTGTTCAGTTTCAGTAAGGCGAGTCTTA	582	
DB	538	CCGCGTGAAGAGCGCGGAGCGCTTCTTTTGTTCAGTTTCAGTAAGGCGAGTCTTA	597	
QY	583	CTTCCACTCCATATTTCTGTGTGAGACACGCGGGGTCAAATTCATGTGTCTGGCGCTT	642	
DB	598	CTTCCACTCCATATTTCTGTGTGAGACACGCGGGGTCAAATTCATGTGTCTGGCGCTT	657	
QY	643	CTGAGTGAAGTTAGCGAGCGAGCTGTGTGACACATCAACGCGGGAGATCGAGCGACCT	702	
DB	658	CTGAGTGAAGTTAGCGAGCGAGCTGTGTGACACATCAACGCGGGAGATCGAGCGACCT	717	
QY	703	GCCCAACTGTGTGCGGTGAGCAAGACCGTAAATGCGCGAGGGGGGAAACAAAGTGT	762	
DB	718	GCCCAACTGTGTGCGGTGAGCAAGACCGTAAATGCGCGAGGGGGGAAACAAAGTGT	777	
QY	763	GAGCAGGTGCTACATCCCAACTACCTCTCTGCGCAAGACTACGCGGAGCTCACTGTGGC	822	
DB	778	GAGCAGGTGCTACATCCCAACTACCTCTCTGCGCAAGACTACGCGGAGCTCACTGTGGC	837	
QY	823	GTGACCTAACTGAGAGGATATTAAGGCGGTTAAACCTGCGCGAGCGCAACCGGT	882	
DB	838	GTGACCTAACTGAGAGGATATTAAGGCGCTGTGTGAACCTTGGCGAGCGCAACCGGT	897	

Qy 883 CGTGGCGCAGACTGAGCCAGCTGAGCAGACCAGAGCAGAAACAAGAAATCTGA 942
Db 898 CGTGGCGCAGACTGAGCCAGCTGAGCCAGACCCAGAGCAGAAACAAGAAATCTGA 957
Qy 943 CCCCAATTTCTGACGCGCTCTGATCCGATCAAAAACTTCGCGACGCTACATGAGCTGAT 1002
Db 958 CCCCAATTTCTGACGCGCTCTGATCCGATCAAAAACTTCGCGCTACATGAGCTGAT 1017
Qy 1003 CGGGGGGCTGGTGGACCGGGGGCATCACTCCGAGAAAGCATGGATCCAGAGAGCAGGC 1062
Db 1018 CGGGGGGCTGGTGGACCGGGGGCATCACTCCGAGAAAGCATGGATCCAGAGAGCAGGC 1077
Qy 1063 CTGATACATCTCTTCAACGCGGCTTCAACTCGGGTCCAGATCAAGGGCGCTTGA 1122
Db 1078 CTGATACATCTCTTCAACGCGGCTTCAACTCGGGTCCAGATCAAGGGCGCTTGA 1137
Qy 1123 CAATGCCGGCAAGATCATGGCGCTGACCAAAATCGGGCCGACCTA CTGGTAGGCCGCG 1182
Db 1138 CAATGCCGGCAAGATCATGGCGCTGACCAAAATCGGGCCGACCTA CTGGTAGGCCGCG 1197
Qy 1183 TCCGCGCCCGCAGATTAAACCAACGCACTTTACCGCATCTTGAGCTGAAGCGCTAGA 1242
Db 1198 TCCGCGCCCGCAGATTAAACCAACGCACTTTACCGCATCTTGAGCTGAAGCGCTAGA 1257
Qy 1243 CCTGCTACGCGCGCTCGTCTTTCTGCGCTGGGCCCGAGAAAGTTTCGAAAAACGCA 1302
Db 1258 ACTGCTACGCGCGCTCGTCTTTCTGCGCTGGGCCCGAGAAAGTTTCGAAAAACGCA 1317
Qy 1303 CACCATCTGCTGTTTGGGGCGGCGCAGCA CGGGCAAGACCAATCGCGAAGCCATCGC 1362
Db 1318 CACCATCTGCTGTTTGGGGCGGCGCAGCA CGGGCAAGACCAATCGCGAAGCCATCGC 1377
Qy 1363 CCAAGCCGTGCGCTTCTACGCTGCTGCTCACTGACCAATGAACTTTCCCTTCAAGA 1422
Db 1378 CCAAGCCGTGCGCTTCTACGCTGCTGCTCACTGACCAATGAACTTTCCCTTCAAGA 1437
Qy 1423 TTGCGTCGACAAAGATGTGTGATCTGGTGGAGAGAGGAGCAAGATGACGGCCAAAGTGTGGA 1482
Db 1438 TTGCGTCGACAAAGATGTGTGATCTGGTGGAGAGAGGAGCAAGATGACGGCCAAAGTGTGGA 1497
Qy 1483 GTCCGCGCAAGGCCATTCTCGGCGGCGAGCAAGGTGCGCTGGA CCAAAAGTGCAGTCTGC 1542
Db 1498 GTCCGCGCAAGGCCATTCTCGGCGGCGAGCAAGGTGCGCTGGA CCAAAAGTGCAGTCTGC 1557
Qy 1543 CGCCCAAGTGCATCCCAACCCCGCTGATGTGTCACTTCCACACCAAGTGTGCGCTGAT 1602
Db 1558 CGCCCAAGTGCATCCCAACCCCGCTGATGTGTCACTTCCACACCAAGTGTGCGCTGAT 1617
Qy 1603 TGAAGGAGAACAGACCACTTTCGAGCACGAGCGCTTGCAGAGCGGATGTTCAAAAT 1662
Db 1618 TGAAGGAGAACAGACCACTTTCGAGCACGAGCGCTTGCAGAGCGGATGTTCAAAAT 1677
Qy 1663 TGAAGTCAACCCGCGCTTGAAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAA 1722
Db 1678 TGAAGTCAACCCGCGCTTGAAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAA 1737
Qy 1723 GTTCTTCCGCTGGGGGCGAGATCAGGTGACGAGTGGCGCATGATTTCTACGATGAAA 1782
Db 1738 GTTCTTCCGCTGGGGGCGAGATCAGGTGACGAGTGGCGCATGATTTCTACGATGAAA 1797
Qy 1783 GGGTGAAGCAACAGACCGGCGCGATGA CGCGGATAAAGCAGAGCCAGCGGGC 1842
Db 1798 GGGTGAAGCAACAGACCGGCGCGATGA CGCGGATAAAGCAGAGCCAGCGGGC 1857
Qy 1843 CTGCGCTCACTCGCGATCATGACGTGACGCGGAGAGAGCTCCGGTGAATTTGC 1902
Db 1858 CTGCGCTCACTCGCGATCATGACGTGACGCGGAGAGAGCTCCGGTGAATTTGC 1917
Qy 1903 CGACAGGATCAAAACAATGTTCTGCTCAGCGGGGCACTTTCAGATGCTGTTCCCTG 1962
Db 1918 CGACAGGATCAAAACAATGTTCTGCTCAGCGGGGCACTTTCAGATGCTGTTCCCTG 1977
Qy 1963 CAAACATGCGAGAGATGAATCAAGATTTTCAACTTTGCTTACGACGAGGAGCCAGAGA 2022

Db 1978 CAAGACATGCGAGAGAAATGAATCAAGATTTTCAACTTTGCTTCAAGCAGCGGAGCAGAGA 2037
Qy 2023 CTGTTCAAGATGTTTCCCGGCTGTCAAGATCTCAACCGGTCTCGAAGAGAGAGCTA 2082
Db 2038 CTGTTCAAGATGTTTCCCGGCTGTCAAGATCTCAACCGGTCTCGAAGAGAGAGCTA 2097
Qy 2083 TCGGAACCTGCTGTCATTCATTCATCTGCTGGGGGGGCTCCCGAGATTTGCTGCTGGG 2142
Db 2098 TCGGAACCTGCTGTCATTCATTCATCTGCTGGGGGGGCTCCCGAGATTTGCTGCTGGG 2157
Qy 2143 CTGCGATCTGCTCAACGTGATCTGATGATGATGTTTCTGAGCAATAATGACTTAAAC 2202
Db 2158 CTGCGATCTGCTCAACGTGATCTGATGATGATGATGTTTCTGAGCAATAATGACTTAAAC 2217
Qy 2203 CAGGTATGCTGCGGATGTTATCTTCCAGATTTGGCTCGAGAGCAACCTCTCTGAGGCA 2262
Db 2218 CAGGTATGCTGCGGATGTTATCTTCCAGATTTGGCTCGAGAGCAACCTCTCTGAGGCA 2277
Qy 2263 TTTGCGAGTGGTGGGACTTTGAAACCTGGAGCCCGGAAACCGAAAGCCAAACGAGCAAAAGC 2322
Db 2278 TTTGCGAGTGGTGGGACTTTGAAACCTGGAGCCCGGAAACCGAAAGCCAAACGAGCAAAAGC 2337
Qy 2323 AGGACGAGCGCGGGGCTTGTGCTTCTGAGCTAACATCTCGAACCTTCAACGAGC 2382
Db 2338 AGGACGAGCGCGGGGCTTGTGCTTCTGAGCTAACATCTCGAACCTTCAACGAGC 2397
Qy 2383 TCGACAGGGGAGCCGCTCAACCGGGCGAGTGCAGCGGCTCTGAGCAGCAAGAGCT 2442
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Qy 2563 TCCAGGCCAAGAGAGGTTCTGAACTTTTGGTCTGGTTGAGAGAGTCTAAGACGG 2622
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Qy 2623 CTCTCGAAGAAAGAACTTCGCTGATGAGCGATGCGCAACAGAGCCAGATCTCTCGGGCA 2682
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Qy 2683 TTTGCGAAGACAGGCGCAGCGCGCTAAGAAAGACTCAATTTTGTGATCAGACTGGCACT 2742
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Qy 2803 GACCTACTCAATGAGCTTTCAGGCGGTGCGCAACCAATGAGCAACATTAACGAAGCGCGG 2862
Db 2818 GACCTACTCAATGAGCTTTCAGGCGGTGCGCAACCAATGAGCAACATTAACGAAGCGCGG 2877
Qy 2863 ACGAGTGGGTAAATGCTCAGAGAAATTTGCAATTTGCAATGCTGAGGCGCAGAG 2922
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Qy 2923 TCATCCACCAACGACCCGAAACATGGGCTTTGCCACTTATTAACAACCACTCTTCAAGC 2982
Db 2938 TCATCCACCAACGACCCGCACTGGGCTTTGCCACTTATTAACAACCACTCTTCAAGC 2997
Qy 2983 AAATCTCAAGTCTTCAACGGGGGCGAGCAACGCAACCACTACTTGGCTACAGCACCC 3042
Db 2998 AAATCTCAAGTCTTCAACGGGGGCGAGCAACGCAACCACTACTTGGCTACAGCACCC 3057
Qy 3043 CTTGGGGATTTTGAATTTCAACAGATTTCCACTGCTCACTTCTCAACAGTGACTGGAGC 3102

Db 3058 CCTGGGGGATTTTGGATTTCACAGATTCCAATGCGCACTTTTTCACACGATGATGCGAGC 3117
Qy 3103 GACTCATCAACAACAAATTTGGGGATTTCCGGCCCAAGAGCTCAACTTCAAGCTTTCAACA 3162
Db 3118 GACTCATCAACAACAAATTTGGGGATTTCCGGCCCAAGAGCTCAACTTCAACTTTCAACA 3177
Qy 3163 TCCAACTCAAGAGAGTCAAGAGATGATGAGCTCAGACCATGCTATTAATCACTTCAACA 3222
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Qy 3583 AGGACTTCTGTTTATGCGCTGAGTCTCAAGCTGAGATGCTGTTCAAGCTTCAAGCTTCAAG 3642
Db 3598 AGGACTTCTGTTTATGCGCTGAGTCTCAAGCTGAGATGCTGTTCAAGCTTCAAGCTTCAAG 3657
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Qy 3763 ACCCTGAG 3822
Db 3778 ACCCTGAG 3837
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Db 3838 GTGTCATGATTTTGGAAAG 3897
Qy 3883 TGATACACAG 3942
Db 3898 TGATACACAG 3957
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Db 3958 CTGTGAG 4017
Qy 4003 TGGGAG 4062
Db 4018 TGGGAG 4077
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Db 4078 GGGGCAAAATTTCTTCAACAG 4137
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Qy 4183 CCGCAGAGATTTTGGGCTACAAAGTTTGTCTTATTCATCAACCCAGATTTCCACAGAGCAAG 4242
Db 4198 CCGCAGAGATTTTGGGCTACAAAGTTTGTCTTATTCATCAACCCAGATTTCCACAGAGCAAG 4257
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Db 4258 TGAAGCTGAGAGATTTGAATGAG 4317
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Db 4438 GTGTTAATCAATTAACCGGTTAATTCGTCAGATGAACTTGGTCTCATGCTCTTATTA 4497
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Db 4498 TCTTATC-GGTTACCATGTTTATGATTAAGCTTACACATTAATCTTGGTGGCTTGGAGATA 4556
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Db 4557 AAAGACTTAAGATGATGAG 4616
Qy 4582 TCGCTGCTCTGAG 4641
Db 4617 TCGCTGCTCTGAG 4676
Qy 4642 GGGCCACAG 4683
Db 4677 GGGCCACAG 4718

RESULT 9
US-10-696-282-1
Sequence 1, Application US/10696282
Publication No. US20040057932A1
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNPVN.031USA
CURRENT FILING DATE: US/10/696,282
PRIOR APPLICATION NUMBER: US/09/807,802A
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4718
TYPE: DNA
ORGANISM: AAV-1
FEATURE:
NAME/KEY: CDS
LOCATION: (335)..(2206)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (2223)..(4430)
OTHER INFORMATION:
US-10-696-282-1

Query Match 90.8%; Score 4253.2; DB 8; Length 4718;

Best Local Similarity 94.7%; Pred. No. 0;				
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;				
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Db	1	TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCCGGGCGCAACCAAGTGGCC	60	
Qy	61	CGAGCCCGGGCTTTGCCCCGGGCGCTCAGTGAAGCGAGCGCGGAGAGAGGAGATG	120	
Db	61	AGACGGCAGAGCTCTGCTCTGCGCGCCACCGAGCGAGCAGCGCGAGAGGAGATG	120	
Qy	121	GCCAACTCCATCACTAGGGGT-----TCCTGAGGGGTGAGTCTGTA	163	
Db	121	GGCAATCCTCATCTAGGGGTATGCGAGCGCTCCCAAGCTGCCCGTCAAGCGCTGA	180	
Qy	164	CGTAAATTAGCTCAATAGGGTTAGGAGGTCTGTATTAGAGTCACTGAGTCT-TTTTGC	222	
Db	181	CGTAAATTAGCTCAATAGGG---GAGTGGTCTGTATTAGTGTCACTGAGTGTCTTTGC	237	
Qy	223	GACATTTTGGACACCAATGNTGTACGCTGGGTATTTAAGCCCGAGTGAACGAGAGGT	282	
Db	238	GACATTTTGGACACCAATGNTGTACATTTAGGGTATATATGAGCGAGTGAAGGAGAT	297	
Qy	283	CTCCATTTTGAAGCGGAGGTTTGAACGCGAGCGCATGCGGGGTTTTCAGAGATTGT	342	
Db	298	CTCCATTTTGAACCGGAAATTGAAACGAGCAGCAGCCATGCGGGCTTCTACGAGTGT	357	
Qy	343	GATTAAAGTCCCGACGACCTTGAACGAGCATCTGCGCGCATTTTCTGAACGCTTTGTAA	402	
Db	358	GATCAAGGTGCGGACGACCTGGAACGAGCATCTGCGCGCATTTTCTGAACGCTTTGTAG	417	
Qy	403	CTGCGTGGCCGAGAAAGAAATGGAGTTGCCCCAGATTCTGACATGATCTGAACTGTAT	462	
Db	418	CTGCGTGGCCGAGAAAGAAATGGAGTGTCCCCGATTTCTACATGATCTGAACTGTAT	477	
Qy	463	TGACAGGACCCCTGACCGTGGCGAGAACTGACGCGCATCTTCTGATCCAATGCGG	522	
Db	478	TGACAGGACCCCTGACCGTGGCGAGAACTGACGCGCATCTTCTGATCCAATGCGG	537	
Qy	523	CCGCGTGAATGAGGCCCGGAGGCCCTCTTCTTTTGTTCAGTTTCAGAAAGGCGAGTCTTA	582	
Db	538	CCGCGTGAATGAGGCCCGGAGGCCCTCTTCTTTTGTTCAGTTTCAGAAAGGCGAGTCTTA	597	
Qy	583	CTTCCACTCCATATTCTGATGAGAACCAAGGGGTGCAATCCATGATGTCGGGCGGTT	642	
Db	598	CTTCCACTCCATATTCTGATGAGAACCAAGGGGTGCAATCCATGATGTCGGGCGGTT	657	
Qy	643	CTTGAATCAGATTGACGACAGCTGATGACACCATCAACGCGGGATTCGAGCGGACCT	702	
Db	658	CTTGAATCAGATTGACGACAGCTGATGACACCATCAACGCGGGATTCGAGCGGACCT	717	
Qy	703	GCCCAACTGTTTCCGCGTGACCAAGACGCGTAATGCGCGGAGGGGGAACAAGTGTGT	762	
Db	718	GCCCAACTGTTTCCGCGTGACCAAGACGCGTAATGCGCGGAGGGGGAACAAGTGTGT	777	
Qy	763	GGAAGATGCTACATCCCACTACTCTCTGCGGCAAGCTACGCGCCGAGCTGCACTGGGC	822	
Db	778	GGAAGATGCTACATCCCACTACTCTCTGCGGCAAGCTACGCGCCGAGCTGCACTGGGC	837	
Qy	823	GTGACTAACATGAGAGAGTATTAAGCGCGTGTTTAACTGCGCCGAGCGCAACGGCT	882	
Db	838	GTGACTAACATGAGAGAGTATTAAGCGCGTGTTTAACTGCGCCGAGCGCAACGGCT	897	
Qy	883	CTGTGGCGACGACTGACCCAGCTGACGACAGCCAGAGAGAGAAATCTGAA	942	
Db	898	CTGTGGCGACGACTGACCCAGCTGACGACAGCCAGAGAGAGAAATCTGAA	957	
Qy	943	CCCCAATTGTAGCGGCGCTGCTCATCCGGTCAAAAACTCCGCAAGCTCATAGAGCTGGT	1002	
Db	958	CCCCAATTGTAGCGGCGCTGCTCATCCGGTCAAAAACTCCGCGGCTCATAGAGCTGGT	1017	
Qy	1003	CGGGTGGCTGTGTGACCGGGGCACTCACTCCGAGAGAGCTGTATCCAGAGAGACAGGC	1062	

Db	1018	CGGGTGGCTGTGTGACCGGGGCACTCACTCCGAGAGAGTGTATCCAGAGAGACAGGC	1077	
Qy	1063	CTGCTACATCTCTTTCACACGCGGCTTCCATCTCGCGGTCTCCAGATCAAGGCGCTTGA	1122	
Db	1078	CTGCTACATCTCTTTCACACGCGGCTTCCATCTCGCGGTCTCCAGATCAAGGCGCTTGA	1137	
Qy	1123	CAATGCGGCAAGATCAATGGGCTGACCAAAATCCGCGCGGAGCTTACCTGTATGAGCGCGC	1182	
Db	1138	CAATGCGGCAAGATCAATGGGCTGACCAAAATCCGCGCGGAGCTTACCTGTATGAGCGCGC	1197	
Qy	1183	TCCGCCCGCGACATTTAAACCAACGCAATTTTACCGATCTCTGAGCTGAACGCTACGA	1242	
Db	1198	TCCGCCCGCGACATTTAAACCAACGCGATTTTACCGATCTCTGAGCTGAACGCTACGA	1257	
Qy	1243	CCCTGCTACGCGCGCTCCGCTCTTCTGCGCTGGGCCAGAAAAGTTTGGAAAACGCA	1302	
Db	1258	ACCTGCTTACCGCGCTCCGCTCTTCTGCGCTGGGCCAGAAAAGTTTGGGAAACGCA	1317	
Qy	1303	CACCATCTGGCTGTTTGGGCGGACACAGGGGCAAGCAACATCCGCGAAGCATGCG	1362	
Db	1318	CACCATCTGGCTGTTTGGGCGGACACAGGGGCAAGCAATCCGCGAAGCATGCG	1377	
Qy	1363	CCACGCGGTGCTTCTTACGCGCTGCTCACTGGAACCAATGGAATCTTCCCTTCAACGA	1422	
Db	1378	CCACGCGGTGCTTCTTACGCGCTGCTCACTGGAACCAATGGAATCTTCCCTTCAATGA	1437	
Qy	1423	TTGCGTGCACAAATGATGATCTGCTGGAGAGAGGCGCAAGATGACGCGCAAGTCTGGA	1482	
Db	1438	TTGCGTGCACAAATGATGATCTGCTGGAGAGAGGCGCAAGATGACGCGCAAGTCTGGA	1497	
Qy	1483	GTCGCGCAAGGCGCATTTCCGCGGCGACAGAGTGGGTGGGACGAAAAGTCAAGTGTGTC	1542	
Db	1498	GTCGCGCAAGGCGCATTTCCGCGGCGACAGAGTGGGTGGGACGAAAAGTCAAGTGTGTC	1557	
Qy	1543	CGCCAGATCGATCCACCCCGGTGATGCTCACTTCCCAACCAATGTGCGCGTGTAT	1602	
Db	1558	CGCCAGATCGATCCACCCCGGTGATGCTCACTTCCCAACCAATGTGCGCGTGTAT	1617	
Qy	1603	TGACGGGAAACAGCACACCTTCCAGCACACGACCGCTTGGAGAACGGATGTTCAAAATT	1662	
Db	1618	TGACGGGAAACAGCACACCTTCCAGCACACGACCGCTTGGAGAACGGATGTTCAAAATT	1677	
Qy	1663	TGAATCAACCGCGGTCTGGAGCATGACTTTGGCAAGGTGCAAAAGCAGAAAGTCAAGA	1722	
Db	1678	TGAATCAACCGCGGTCTGGAGCATGACTTTGGCAAGGTGCAAAAGCAGAAAGTCAAGA	1737	
Qy	1723	GTTCTTCCGCTGGCGGAGATCACTGACGAGTGGCGGATGATGATTCACTCAAGAA	1782	
Db	1738	GTTCTTCCGCTGGCGGAGATCACTGACGAGTGGCGGATGATGATTCACTCAAGAA	1797	
Qy	1783	GGGTGAGCCCAACACAGACCCGCGGATGACCGGATTAAGCGAGCCCAAGCGGCGC	1842	
Db	1798	GGGTGAGCCCAACACAGACCCGCGGATGACCGGATTAAGCGAGCCCAAGCGGCGC	1857	
Qy	1843	CTGCCCCCTAGTGGCGGATCACTGACGTCAAGCGGAGAGACTCGGTTGCACTTTGCG	1902	
Db	1858	CTGCCCCCTAGTGGCGGATCACTGACGTCAAGCGGAGAGACTCGGTTGCACTTTGCG	1917	
Qy	1903	CGACAGGTACCAAAACAAATGTTCTCGTCAAGCGGAGATGTTTCAATGCTTCCCTG	1962	
Db	1918	CGACAGGTACCAAAACAAATGTTCTCGTCAAGCGGAGATGTTTCAATGCTTCCCTG	1977	
Qy	1963	CAAAACATGGAGAGAAATGAATCAGAATTTTCAATTTGCTTTCACGCAAGGAGACAGGA	2022	
Db	1978	CAAAACATGGAGAGAAATGAATCAGAATTTTCAATTTGCTTTCACGCAAGGAGACAGGA	2037	
Qy	2023	CTGTTCAAGATGTTTCCCGGCGGTGACAGATCTCAACCGGTGCTGAGAAAGAGAGCTA	2082	
Db	2038	CTGTTCAAGATGTTTCCCGGCGGTGACAGATCTCAACCGGTGCTGAGAAAGAGAGCTA	2097	
Qy	2083	TGGGAAACTCTGTGCACTTATCATCTGCTGGGCGGGGCTCCGAGATTGCTTGTCTGGC	2142	
Db	2098	TGGGAAACTCTGTGCACTTATCATCTGCTGGGCGGGGCTCCGAGATTGCTTGTCTGGC	2157	

Oy 2143 CTGGATCTGGTCAACGCGATCTGGATGACGTGTTCTGAGCAATTAATGACTTAAAC 2202
Db 2158 CTGGATCTGGTCAACGCGATCTGGATGACGTGTTCTGAGCAATTAATGACTTAAAC 2217
Oy 2203 CAGGATAGGCTGCGGATGGTTATCTTCCAGATTGGCTGAGAGCAACCTCTCTGAGGCA 2262
Db 2218 CAGGATAGGCTGCGGATGGTTATCTTCCAGATTGGCTGAGAGCAACCTCTCTGAGGCA 2277
Oy 2263 TTCCGCAATGGTGGGACTTGAATCTGGAGCCCGAAACCCAAAGCCCAACGCAAAAAGC 2322
Db 2278 TTCCGCAATGGTGGGACTTGAATCTGGAGCCCGAAACCCAAAGCCCAACGCAAAAAGC 2337
Oy 2323 AGAGCAAGCGCCGGGGTCTGGTCTTCTGGCTACAAATACCTGGAACCTTCAACGAGC 2382
Db 2338 AGAGCAAGCGCCGGGGTCTGGTCTTCTGGCTACAAATACCTGGAACCTTCAACGAGC 2397
Oy 2383 TCAGCAAGGGGAGCCGCTCAACCGGCGGATGCAAGCGGCCCTCGAGCAAGCAAGGCT 2442
Db 2398 TCAGCAAGGGGAGCCGCTCAACCGGCGGAGCGAGCGGCCCTCGAGCAAGCAAGGCT 2457
Oy 2443 ACAGCAAGCACTCAAAAGCGGCTGACATCCGTAACCTGGTATTAACAAGCCGAGCGCG 2502
Db 2458 ACAGCAAGCACTCAAAAGCGGCTGACATCCGTAACCTGGTATTAACAAGCCGAGCGCG 2517
Oy 2503 AGTTTCAGGAGCGCTCTGCAAGAAGATAGTCTTTTGGGGGCAACCTCGGGGAGCACT 2562
Db 2518 AGTTTCAGGAGCGCTCTGCAAGAAGATAGTCTTTTGGGGGCAACCTCGGGGAGCACT 2577
Oy 2563 TCACAGGCCAAGAAGGGTTTCGAACCTTTTGTCTGTGTGAGGAGGCTTAAGACGG 2622
Db 2578 TCACAGGCCAAGAAGGGTTTCGAACCTTTGTGTGTGAGGAGGCTTAAGACGG 2637
Oy 2623 CTCCTGGAATAAAGCTGCGGTAAGAGCGAGCGCAAGAGCCGACCTCTCTCGGCA 2682
Db 2638 CTCCTGGAATAAAGCTGCGGTAAGAGCGAGCGCAAGAGCCGACCTCTCTCGGCA 2697
Oy 2683 TTGGCAAGACAGGCGAGCGCCGCTAAAGAGACTCAATTTGTGAGACTGGGCACT 2742
Db 2698 TTGGCAAGACAGGCGAGCGCCGCTAAAGAGACTCAATTTGTGAGACTGGGCACT 2757
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Db 2758 CAGAGTCAGTCCCGGACCCCAACCTCTCGAGAACTTCACGCAACCCCGCTGTGG 2817
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Db 2878 ACGGATGGGTAAATGCTCAGGAAATTGGCAATTCATTCACATGCTGGGCGACAGAG 2937
Oy 2923 TCATACCAACCAAGCAAGGCTTGGCCCACTTAACAACCACTCTCAAGC 2982
Db 2938 TCATACCAACCAAGCAAGGCTTGGCCCACTTAACAACCACTCTCAAGC 2997
Oy 2983 AAATCTCCAGTCTTCAAGGGGGGCAAGCAAGCAACCACTTGGGCTAAGCAAGC 3042
Db 2998 AAATCTCCAGTCTTCAAGGGGGGCAAGCAAGCAACCACTTGGGCTAAGCAAGC 3057
Oy 3043 CTTGGGGGTATTTGATTTTCAACAGATTCACTGCAATTTCTCAACGATGCTGGAGC 3102
Db 3058 CTTGGGGGTATTTGATTTTCAACAGATTCACTGCAATTTCTCAACGATGCTGGAGC 3117
Oy 3103 GACTCATCAACAACATTTGGGATTCGGGCCAAGAGACTCAACTTCAAGCTCTTCAACA 3162
Db 3118 GACTCATCAACAACATTTGGGATTCGGGCCAAGAGACTCAACTTCAAGCTCTTCAACA 3177
Oy 3163 TCCAAGTCAAGGAGTCAAGCAATGATGGGTCAAGCAATGGCTTAATTAACCTTACCA 3222
Db 3178 TCCAAGTCAAGGAGTCAAGCAATGATGGGTCAAGCAATGGCTTAATTAACCTTACCA 3237

Oy 3223 GCAAGGTTCAAGTCTTGTCCGACTCCGAGTACCAAGTCCCGTACGTCCTGGCTCGCG 3282
Db 3238 GCAAGGTTCAAGTCTTGTCCGACTCCGAGTACCAAGTCCCGTACGTCCTGGCTCGCG 3297
Oy 3283 ACCAGGCTGCTCCCTCCGTTCCCGGCAAGCTTTCATGATTCGCACTAGGCTTACC 3342
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Oy 3343 TAAAGCTCAACAAATGGAGCGCAGGCAATGGGAGCTCATCTTTTACCTGCTGGATATT 3402
Db 3358 TAAAGCTCAACAAATGGAGCGCAGGCAATGGGAGCTCATCTTTTACCTGCTGGATATT 3417
Oy 3403 TCCCATGCAAGTCTGAGAACGGGCAATTAATCTTACCTTACGTAACCTTGGAGAGC 3462
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Oy 3523 TCAGCCAGTACCTGTATTACCTGAACAGAACTCAACATCAGTCCGGAATGCCAANA 3582
Db 3538 TCAGCCAGTACCTGTATTACCTGAACAGAACTCAACATCAGTCCGGAATGCCAANA 3597
Oy 3583 AGGACTGCTGTTTACCGCTGGGTCTTCAAGCTGCAATGTCGTTCAAGCCCAAAACCTGGC 3642
Db 3598 AGGACTGCTGTTTACCGCTGGGTCTTCAAGCTGCAATGTCGTTCAAGCCCAAAACCTGGC 3657
Oy 3643 TACCTGAGCCCTGTTACCGGCAAGCGGCTTTCTAAACAAACCAAGCAACCAACA 3702
Db 3658 TACCTGAGCCCTGTTTACCGGCAAGCGGCTTTCTAAACAAACCAAGCAACCAACA 3717
Oy 3703 GCAACTTACCTGGACTGCTGCTTCAAAATATTAACCTTAATGGGCGGATCTATAATCA 3762
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Oy 3763 ACCCTGCACTGCTATGCTCTCAACAAAGCAAGCAAGCAAGTCTTCCATGAGCG 3822
Db 3778 ACCCTGCACTGCTATGCTCTCAACAAAGCAAGCAAGCAAGTCTTCCATGAGCG 3837
Oy 3823 GTGTCATGATTTTGGAAAGAGAGCGCGGAGCTTCAACACTGCTTTGGACATATCA 3882
Db 3838 GTGTCATGATTTTGGAAAGAGAGCGCGGAGCTTCAACACTGCTTTGGACATATCA 3897
Oy 3883 TGATCAAGAGAGAGAGAAATCAAGCACTAAACCCGCTGGCCACGGAAGATTTGGGA 3942
Db 3898 TGATCAAGAGAGAGAGAAATCAAGCACTAAACCCGCTGGCCACGGAAGATTTGGGA 3957
Oy 3943 CTGTGCAATCTTCAAGAGCAAGCAAGACCTGTGACCGGAGATGTGCATGTTA 4002
Db 3958 CTGTGCAATCTTCAAGAGCAAGCAAGACCTGTGACCGGAGATGTGCATGTTA 4017
Oy 4003 TGGAGGCTTACCTGGAAATGTGTGGCAAGACAGACCTTAATCTGCAAGGCTTATTT 4062
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Oy 4063 GGGCCAAATTTCTCAACAGGATGACATTTACCCGCTCTCTCATGGGCGGCTTTG 4122
Db 4078 GGGCCAAATTTCTCTCAACAGATGACATTTTACCCGCTCTCTCTTATGGGCGGCTTTG 4137
Oy 4123 GACTTAAGCAACCGGCTCTCAATCTCATTAATAAAACAGCGCTGTTCTGCAATCTC 4182
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Db 4258 TGAGCTGAGATTTGAATGGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCCGAAG 4317
Oy 4303 TGAGATTAATCTTAATGCAAAATCTGCAACGTTGATTTCACTGTGGAACAATG 4362

Db 4318 TGCAGTACACATCCAAATTATGCAAAATCTGCCAAGTTGATTTTACTGTGGACAACANAG 4377
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Db 4378 GACTTAAATCTAGAGCTTGCCTCCCATTTGGACCCGTTACTCAACCGTCCCTGTAAATAC 4437
Qy 4423 GTGTTAATCAATTAACCGGTTAATCGTGTAGTTGAACCTTGTGTATGCTATGCTATTA 4482
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Qy 4541 -----ATACCTCTAGTATGATGAGTTGCCACTCCCTCTATGCGGCG 4581
Db 4557 AAAGACTTACGTATCGGATTAACCCCTAGTATGAGTTGCCACTCCCTCTCTGCGGCG 4616
Qy 4582 TCGCTCGCTCGGTGGGGCGGCGAGAGAGCTGCGGTGCGGAGACCTTTGGTCCGCA 4641
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Qy 4642 GAGCCACCGAG 4683
Db 4677 GAGCCACCGAG 4718

RESULT 10
US-10-696-900-1
Sequence 1, Application US/10696900
Publication No. US20040057933A1
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
FILE REFERENCE: GNPVN 031USA
CURRENT APPLICATION NUMBER: US/10/696,900
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US/09/807,802A
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PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4718
TYPE: DNA
ORGANISM: AAV-1
FEATURE:
NAME/KEY: CDS
LOCATION: (335)..(2206)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (2223)..(4430)
OTHER INFORMATION:
US-10-696-900-1

Query Match 90.8%; Score 4253.2; DB 8; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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Db 61 AGAGCGGAGAGCTGCTGCTGCGGCGGCGCAACGAGCGAGCGCGCGAGAGAGAGTG 120

Qy 121 GCCAATCTCATCACTAGGGGT-----TCCTGAGAGGGGTGAGTCGTGA 163
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Qy 164 CGTGAATTAAGTATAGGGGTATAGGGAGTCTGTATTAAGAGTCACTGAGTGA--TTTTC 222
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Qy 403 CTGGGTGGCGGAG 462
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Qy 463 TGAGAGGCAACCCCTGACCCGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
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Qy 523 CCGGCTGAGTAAAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 582
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Db 718 GCCCAATCTGTTCCGCGTGAACCAAGAGCGGTAATGCGCGGAGAGAGAGAGAGAGAG 777
Qy 763 GAGAGAGTGAATCTCCCAATCTAATCTTCCGCGGAGAGAGAGAGAGAGAGAGAGAG 822
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Qy 1003 CGGCTGCTGCTGAG 1062
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Qy 1063 CTCGTACATCTCTTCAACGCGGCTTCAACTCGCGGTCCAGATCAAGGCGGCTGTGA 1122
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Qy 1303 CACCATCGGCTGTTTGGGGCGGSCACCACGGGCAAGCAACATCCGCGGAAGCATCGC 1362
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Qy 1663 TGAATCTCACCCGCGCTGAGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1722
Db 1678 TGAATCTCACCCGCGCTGAGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1737
Qy 1723 GTTCTTCGCTGGGCGAGATCAAGTGAACGAGTGGCGCATGATTTCTACGTCAAGAA 1782
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Qy 1783 GGGTGAAGCCAAACAAGACCCGCCGATGAGCGGATTAAGCCGAGCCCAAGCGGCG 1842
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Qy 1843 CTGCCCCCTCAGTCCGAGTCCATGCAAGTCAAGCGGGAAGAGTCCGAGTGAATTGGC 1902
Db 1858 CTGCCCCCTCAGTCCGAGTCCATGCAAGTCAAGCGGGAAGAGTCCGAGTGAATTGGC 1917
Qy 1903 CGACAGGTACCAAAACAATGTTCTGTCACGCGGGCATGCTTCAGATGCTGTTCCCTG 1962
Db 1918 CGACAGGTACCAAAACAATGTTCTGTCACGCGGGCATGCTTCAGATGCTGTTCCCTG 1977
Qy 1963 CAAAACATGCAAGAGAAATGAATCAGAAATTTCAACATTTGCTTCAACGCGGACAGAGA 2022
Db 1978 CAAAACATGCAAGAGAAATGAATCAGAAATTTCAACATTTGCTTCAACGCGGACAGAGA 2037
Qy 2023 CTGTTCAGAATGTTTCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGAGCTA 2082
Db 2038 CTGTTCAGAATGTTTCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGAGCTA 2097
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Qy 2203 CAGGATATGCTGCGATGATCTTCCAGATTTGGCTGAGAGCAACCTCTCTGAGGCA 2262
Db 2218 CAGGATATGCTGCGATGATCTTCCAGATTTGGCTGAGAGCAACCTCTCTGAGGCA 2277
Qy 2263 TTCCGCAATGCTGGAGCTTGAACCTTGAGCCCGCAACCCAAAGCCAAACGAGAAAAAGC 2322

Db 2278 TTCCGCAATGCTGGAGCTTGAACCTTGAGCCCGCAACCCAAAGCCCAACGAGAAAAAGC 2337
Qy 2323 AGGACGACCGCCGGGGCTGTGGTCTTCTGCTTCAAGATACCTTCGACCCCTTCAACGAC 2382
Db 2338 AGGACGACCGCCGGGGCTGTGGTCTTCTGCTTCAAGATACCTTCGACCCCTTCAACGAC 2397
Qy 2383 TCGACAGGGGGAGCCCGTCAACGCGGCGATGACGCGGCTCTGAGCAAGAGGCT 2442
Db 2398 TCGACAGGGGGAGCCCGTCAACGCGGCGATGACGCGGCTCTGAGCAAGAGGCT 2457
Qy 2443 ACGACAGGAGCTCAAGCGGGTGAACATCTGACCTGCGGTATTAACACGCGGACCGC 2502
Db 2458 ACGACAGGAGCTCAAGCGGGTGAACATCTGACCTGCGGTATTAACACGCGGACCGC 2517
Qy 2503 AGTTTCAGAGCGCTTCGCAAGAGATACGCTTTTGGGGGCAACCTCGGCGAGAGCTC 2562
Db 2518 AGTTTCAGAGCGCTTCGCAAGAGATACGCTTTTGGGGGCAACCTCGGCGAGAGCTC 2577
Qy 2563 TCCAGGCCAAGAAAGAGGTTCTCGAACCTTTGCTGTGTGAGAAAGTGTAAAGACG 2622
Db 2578 TCCAGGCCAAGAAAGCGGTTCTCGAACCTCTCGACTCTCGGTGTGAGAAAGGCTTAAGACG 2637
Qy 2623 CTCTGGAAAGAAACGTCGCTGTAAGCAATGCTCCAGAAACCTCCAGAACCTCTCTCGGCA 2682
Db 2638 CTCTGGAAAGAAACGTCGCTGTAAGCAATGCTCCAGAAACCTCCAGAACCTCTCTCGGCA 2697
Qy 2683 TTGGCAAGACAGGCGAGCAGCCCGCTTAAAGAGACTCATTTTGGTCAACCTGGGCACT 2742
Db 2698 TTGGCAAGACAGGCGAGCAGCCCGCTTAAAGAGACTCATTTTGGTCAACCTGGGCACT 2757
Qy 2743 CAGAGTCAGTCCCGCACCCCAACCTCTCGAGAACTCCAGAACCTCCGCTGCTGTGG 2802
Db 2758 CAGAGTCAGTCCCGCACCCCGAGTCCCAACCTCTCGAGAACTCCAGAACCTCCGCTGCTGTGG 2817
Qy 2803 GACCTTACTAATATGCTTCAAGCGGTGGCGCAACATGCGACATATACGAAGCGCGC 2862
Db 2818 GACCTTACTAATATGCTTCAAGCGGTGGCGCAACATGCGACATATACGAAGCGCGC 2877
Qy 2863 ACGAGTGGGTAAATGCTTCAGGAAATTGGGATTTGCGATTCCACATGGCTGGGAGACAG 2922
Db 2878 ACGAGTGGGTAAATGCTTCAGGAAATTGGGATTTGCGATTCCACATGGCTGGGAGACAG 2937
Qy 2923 TCAATCAACAACAGACCCGGAACATGGGCTTGGCCACTTAAACAACAACCTCTCAAGC 2982
Db 2938 TCAATCAACAACAGACCCGGAACATGGGCTTGGCCACTTAAACAACAACCTCTCAAGC 2997
Qy 2983 AAATCTCAATGCTTCAACGGGGCCAGCAACACCACTACTTCGCTACAGCACCC 3042
Db 2998 AAATCTCAATGCTTCAACGGGGCCAGCAACACCACTACTTCGCTACAGCACCC 3057
Qy 3043 CTTGGGGGTAAATTTTGAATTTCAAGATTTCACTGCCATTTCTACACAGTGACTGGAGC 3102
Db 3058 CTTGGGGGTAAATTTTGAATTTCAAGATTTCACTGCCATTTCTACACAGTGACTGGAGC 3117
Qy 3103 GACTCATCAACAACAATTTGGGGAATTCGGGCCAAGAGACTCAACTTCAACCTCTTCAACA 3162
Db 3118 GACTCATCAACAACAATTTGGGGAATTCGGGCCAAGAGACTCAACTTCAACCTCTTCAACA 3177
Qy 3163 TCCAGTCAAGAGGTCAACGATATATGGCTCACGACCATGCTAATATACCTTAACA 3222
Db 3178 TCCAGTCAAGAGGTCAACGATATATGGCTCACGACCATGCTAATATACCTTAACA 3237
Qy 3223 GCAAGGTTCAAGCTTGTGGGACGCGGATACAGATTCGCTGCGTCCGCTGCGC 3282
Db 3238 GCAAGGTTCAAGCTTGTGGGACGCGGATACAGATTCGCTGCGTCCGCTGCGC 3297
Qy 3283 ACGAGGCTGCTCCCTCCGTCGCGGAGAGTGTTCATGATTTCCGACATGCGCTAAC 3342
Db 3298 ACGAGGCTGCTCCCTCCGTCGCGGAGAGTGTTCATGATTTCCGACATGCGCTAAC 3357
Qy 3343 TTAAGCTCAACAATGGCAGCAGGCAAGTGGAGCGCTCATCTTTTACTGCTGGAATAT 3402

OY 403 CTGGGTGGCCGAGAGGAATGGAGTTGCCGCAAGATTCTGACATGATGATCTGATCTGAT 462
DB 418 CTGGGTGGCCGAGAGGAATGGAGTTGCCGCAAGATTCTGACATGATGATCTGATCTGAT 477
OY 463 TGAAGAGGACACCCCTGACCGTGGCCGAGAAAGCTGACGCGCACTTCTTGCTCACTGGCG 522
DB 478 TGAAGAGGACACCCCTGACCGTGGCCGAGAAAGCTGACGCGCACTTCTTGCTCACTGGCG 537
OY 523 CCGGCTGATGAAGGCCCCCGAGGCCCCCTTCTTGTGTAGTTTCCAGAAAGGCGAGTCTTA 582
DB 538 CCGGCTGATGAAGGCCCCCGAGGCCCCCTTCTTGTGTAGTTTCCAGAAAGGCGAGTCTTA 597
OY 583 CTTCCACCTCCATATTTCTGTGAGAGACCAAGGAGGCTCAATTCATGAGTGTGGGCGGCTT 642
DB 598 CTTCCACCTCCATATTTCTGTGAGAGACCAAGGAGGCTCAATTCATGAGTGTGGGCGGCTT 657
OY 643 CTTGATGATGATTAAGGCAAGAGTGGTCAAGCACTTACCGGAGATCGAGCCGACCTT 702
DB 658 CTTGATGATGATTAAGGCAAGAGTGGTCAAGCACTTACCGGAGATCGAGCCGACCTT 717
OY 703 GCCCAACTGTTTCCGGGTGACCAAGACGCTTAATGGCCCGGAGGGGGGAAACAAGTGGT 762
DB 718 GCCCAACTGTTTCCGGGTGACCAAGACGCTTAATGGCCCGGAGGGGGGAAACAAGTGGT 777
OY 763 GGAAGAGTGTACATCCCACTACCTCTGGCCCAAGACTAGCCGAGCTGCAGTGGGC 822
DB 778 GGAAGAGTGTACATCCCACTACCTCTGGCCCAAGACTAGCCGAGCTGCAGTGGGC 837
OY 823 GTGACATGACATGAGAGATATATAGCGCGTGTAAACCTTGAGCGCAACCGGCT 882
DB 838 GTGACATGACATGAGAGATATATAGCGCGTGTAAACCTTGAGCGCAACCGGCT 897
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DB 898 GGTGGCCGACGACCTGACCCACGTCAGCCAGACCCAGAGAGCAAGAGGAATCTGAA 957
OY 943 CCCCATTCTGACGCGGCTGTCACTCCGGTCAAAAACTCCGCAAGCTCATGAGAGTGGT 1002
DB 958 CCCCATTCTGACGCGGCTGTCACTCCGGTCAAAAACTCCGCGCGCTCATGAGAGTGGT 1017
OY 1003 CGGGTGGCTGTGACCGGGGCGATCACTCCGAGAAAGTGGATCGAAGAGACCAAGGC 1062
DB 1018 CGGGTGGCTGTGACCGGGGCGATCACTCCGAGAAAGTGGATCGAAGAGACCAAGGC 1077
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DB 1078 CTCGACATCTCTTCAACGCGCCTCCCACTCCGGGCTCCAGATCAAGGCGCTTGGGA 1137
OY 1123 CAATGCGCGCAAGATCATGCGCTGACCAAAATCCGCGCCGCACTACCTGTAGAGCCCGC 1182
DB 1138 CAATGCGCGCAAGATCATGCGCTGACCAAAATCCGCGCCGCACTACCTGTAGAGCCCGC 1197
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DB 1318 CACCATCTGAGCTGTTTGGGCGCGGCAACCAAGGCAACCAATCCGCGAAGCCATGCG 1377
OY 1363 CCAAGCGCTGCTCTTCAAGGCTGCTGTAATGACCAATGAGAACTTTCCCTTCAACGA 1422
DB 1378 CCAAGCGCTGCTCTTCAAGGCTGCTGTAATGACCAATGAGAACTTTCCCTTCAACGA 1437
OY 1423 TTGGGTGACAAAGATGATGATCTGGTGGAGGAGGAGCAAGATGACGGGCAAGGCTGTGGA 1482
DB 1438 TTGGGTGACAAAGATGATGATCTGGTGGAGGAGGAGCAAGATGACGGGCAAGGCTGTGGA 1497

OY 1483 GTCCGCCAAGGCCATTTCTCGGCGGCAAGAGTGGCGGTGGAGCCAAAAAGTGACGTGTC 1542
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OY 1543 CGCCAGATGATATCCACCCCCGTGATGCTCACTCTCCAACAACCAACTGTGCGCGGTGAT 1602
DB 1558 CGCCAGATGATATCCACCCCCGTGATGCTCACTCTCCAACAACCAACTGTGCGCGGTGAT 1617
OY 1603 TGAAGGGAACAGACCAACCTTTCGAGCAACAGACCGGTTGACAGAACCGAGTTCAAATT 1662
DB 1618 TGAAGGGAACAGACCAACCTTTCGAGCAACAGACCGGTTGACAGAACCGAGTTCAAATT 1677
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OY 1723 GTTCTTCCGCTGGGCGGAGATCACTGACACGAGGTGGCCGATGAGTTCCTAAGTCAAGAA 1782
DB 1738 GTTCTTCCGCTGGGCGGAGATCACTGACACGAGGTGGCCGATGAGTTCCTAAGTCAAGAA 1797
OY 1783 GGGTGGAGCCAAACAAGACCCGCCCCGATGACGCGGATTAAGCGAGCCCAAGCGGGC 1842
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OY 1843 CTGCCCCCTCAGTGCGGATCCATGACGTGACACGCGGAAGAGCTCCGGTGAACCTTTCG 1902
DB 1858 CTGCCCCCTCAGTGCGGATCCATGACGTGACACGCGGAAGAGCTCCGGTGAACCTTTCG 1917
OY 1903 CGACAGGTACCAAAACAATGTTTCTGTCACGCGGGGATAGCTTCAAGTGTCTTCCCTG 1962
DB 1918 CGACAGGTACCAAAACAATGTTTCTGTCACGCGGGGATAGCTTCAAGTGTCTTCCCTG 1977
OY 1963 CAATAATGCGAAGATGATGATCAATTTCAACTTGTGCTTCAACGACCGGACCAAGAGA 2022
DB 1978 CAATAATGCGAAGATGATGATCAATTTCAACTTGTGCTTCAACGACCGGACCAAGAGA 2037
OY 2023 CTGTTCAGAAATGTTTCCCGCGCGTGTCAAGATCTCAACCGGTGTCAAGAAAGACGTA 2082
DB 2038 CTGTTCAGAAATGTTTCCCGCGCGTGTCAAGATCTCAACCGGTGTCAAGAAAGACGTA 2097
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DB 2158 CTGCGATCTGGTCAACGTGATCTGATGACTGTGTTCGAGCAATTAATGACTTAAAC 2217
OY 2203 CAGGTATGCTGCCGATGGTTATCTTCAGATTGGCTCGAGAACCACTCTGAGGGCA 2262
DB 2218 CAGGTATGCTGCCGATGGTTATCTTCAGATTGGCTCGAGAACCACTCTGAGGGCA 2277
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DB 2278 TTGCGCAGTGTGGGACTTTGAAACCTGGAAGCCCCGAAAGCCCAAGCAAGCAAGAAAGC 2337
OY 2323 AGAGCAGACGCGCGGGGTCTGGTGTCTCTGAGTCAAGTACTCTGAGACCTTCAACGAGC 2382
DB 2338 AGAGCAGACGCGCGGGGTCTGGTGTCTCTGAGTCAAGTACTCTGAGACCTTCAACGAGC 2397
OY 2383 TCGACAAAGGGAGACCCGCTCAACGCGCGGATGACGCGCCTTGAGACGACAAAGGCT 2442
DB 2398 TCGACAAAGGGAGACCCGCTCAACGCGCGGATGACGCGCCTTGAGACGACAAAGGCT 2457
OY 2443 ACGACAGCAGCTCAAGCGCGGTGACAAATCCGTAACCTGCGGTATTAACAGCGCGACGCG 2502
DB 2458 ACGACAGCAGCTCAAGCGCGGTGACAAATCCGTAACCTGCGGTATTAACAGCGCGACGCG 2517
OY 2503 AGTTTCAGAGAGCGCTGCAAGAAAGATACGCTTTTGGGGCAACCTCGGCGAGCAGTCT 2562
DB 2518 AGTTTCAGAGAGCGCTGCAAGAAAGATACGCTTTTGGGGCAACCTCGGCGAGCAGTCT 2577
OY 2563 TCCAGGCCAAAGAGGGTCTTCGAACCTTTTGGTCTGTTGAGAAAGGTGCTAAGAGCG 2622

Db 2578 TCCAGGCCAAGAGGGGTTCTCGAACCCTCGGTCTGGTTAGAGAGGCGCTAAGACGG 2637
Qy 2623 CTCCTGGAAGAAAGCTCCGGTAGAGACAGTGCACAAGAGCCAGACTCTCTCGGGCA 2682
Db 2638 CTCCTGGAAGAAAGCTCCGGTAGAGAGTGCACAAGAGCCAGAAGCTCTCTCGGGCA 2697
Qy 2663 TTGGCAAGACAGGCGAGAGCCCGCTAAAGAGCTCAATTTTGTGAGATTGGCGACT 2742
Db 2698 TCGGCAAGACAGGCGAGAGCCCGCTAAAGAGACTCAATTTTGTGAGACTGGCGACT 2757
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Qy 2923 TCATCACCAACGACACCCGAAATGAGGCTTGGCCACTTAACAACCACTCTACAAAGC 2982
Db 2938 TCATCACCAACGACACCCGACCTGGGCTTGGCCACTTAACAATACCACTCTACAAAGC 2997
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Db 2998 AAATCTCGAGTCTTCAACGGGGGCGCAGCAACCAACCACTTCTGGCTACAGACCC 3057
Qy 3043 CCTGGGGTATTTTAAATTTTCAACAGATTTCATCTGCATTTCTACACAGTGACTGGCAGC 3102
Db 3058 CCTGGGGTATTTTAAATTTTCAACAGATTTCATCTGCATTTCTACACAGTGACTGGCAGC 3117
Qy 3103 GACTCATCAACAACATTTGGGGATTCCGGGCCCAAGAGACTCACTTCAAGCTCTTCAACA 3162
Db 3118 GACTCATCAACAACATTTGGGGATTCCGGGCCCAAGAGACTCACTTCAAGCTCTTCAACA 3177
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Db 3178 TCCAAAGTCAAGAGGTCAAGAGATGATGGCGTACAGACCAATCGCTAATAACCTTACCA 3237
Qy 3223 GCAAGGTTCAAGTCTTTGTCGACTCGAGTACCAATGCCGTACCTCGGCTCTGGCG 3282
Db 3238 GCAAGGTTCAAGTCTTTGTCGACTCGAGTACCAATGCCGTACCTCGGCTCTGGCG 3297
Qy 3283 ACCAGGGGTGCTCCCTCGGTTCCGGGCGGAGCTGTTCAATGATTCGCGAATACGGCTAC 3342
Db 3298 ACCAGGGGTGCTCCCTCGGTTCCGGGCGGAGCTGTTCAATGATTCGCGAATACGGCTAC 3357
Qy 3343 TAAAGCTCAACAATGGACAGCCAGGAGTGGAGCGCTACCTTTTACTGCTGAATATTT 3402
Db 3358 TGAAGCTCAACAATGGACAGCCAGGAGTGGAGCGCTACCTTTTACTGCTGAATATTT 3417
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Db 3418 TCCCTTCTCAGATGCTGAGAAAGGGCAACATTTTACTGCTACACTTTCGAGAGAG 3477
Qy 3463 TGCCTTTCCACAGAGCTACAGCGCAAGCCAGAGCTGGACCGGCTGATGAATCTCTCA 3522
Db 3478 TGCCTTTCCACAGAGCTACAGCGCAAGCCAGAGCTGGACCGGCTGATGAATCTCTCA 3537
Qy 3523 TCGACCAATACCTGTATTAATCTGAAACAGAACTCACAAATCAATCGGAAAGTCCCAACA 3582
Db 3538 TCGACCAATACCTGTATTAATCTGAAACAGAACTCACAAATCAATCGGAAAGTCCCAACA 3597
Qy 3583 AGGACTTCTGTTTAGCGGTGGGTCTCAAGCTGGCATGTGTTCAGCCCAAAAACCTGAC 3642
Db 3598 AGGACTTCTGTTTAGCGGTGGGTCTCAAGCTGGCATGTGTTCAGCCCAAAAACCTGAC 3657
Qy 3643 TACCTGACCCCTGTTTACCGGCGAGAGCGGTTCTTAAACAAAACAGACAAACAACA 3702

Db 3658 TACCTGACCCCTGTTATCGGAGAGAGCGGTTTCTTAAACAAAACAGACAAACAACA 3717
Qy 3703 GCAACTTTAATCTGGAGCTGGTCTTCAAAATTAACCTTAATAGGCGGTAAATCTTAATCA 3762
Db 3718 GCAATTTTAATCTGGAGCTGGTCTTCAAAATTAACCTTAATAGGCGGTAAATCTTAATCA 3777
Qy 3763 ACCCTGACCTGATAGGCTCAACAAGAGAGCAAAAGACAAAGTCTTTTCCCATAGAGC 3822
Db 3778 ACCCTGACCTGATAGGCTCAACAAGAGAGCAAAAGACAAAGTCTTTTCCCATAGAGC 3837
Qy 3823 GTGTATGATTTTGAAGAGAGAGCGCGGAGCTTCAACAATGATGAGCAATGTCAC 3882
Db 3838 GTGTATGATTTTGAAGAGAGAGCGCGGAGCTTCAACAATGATGAGCAATGTCAC 3897
Qy 3883 TGATACAGAGAGAGAGAAATCAAGGCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942
Db 3898 TGATACAGAGAGAGAGAAATCAAGGCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3957
Qy 3943 CTGTGGCAGTCAATCTCCAGAGCAGAGCAGACAGACCCCTGGAGCCGAGATGTGATGTA 4002
Db 3958 CTGTGGCAGTCAATCTCCAGAGCAGAGCAGACAGACCCCTGGAGCCGAGATGTGATGTA 4017
Qy 4003 TGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGAGTATACCTGACAGGCTCTATTT 4062
Db 4018 TGGAGCCTTACCTGGAATGGTGTGGCAAGAGTATACCTGACAGGCTCTATTT 4077
Qy 4063 GGGCCAAATTTCTCACAGGATGGAACCTTACCCGCTCTCTCATGAGCGGCTTTG 4122
Db 4078 GGGCCAAATTTCTCACAGATGGAACCTTACCCGCTCTCTCATGAGCGGCTTTG 4137
Qy 4123 GACTTAAGCAGCCGCTCTCAGATCCCTCAATCAAAAACAGCGCTGTTCTGGAATCCGC 4182
Db 4138 GACTTAAGCAGCCGCTCTCAGATCCCTCAATCAAAAACAGCGCTGTTCTGGAATCCGC 4197
Qy 4183 CGGAGAGTTTTTGGCTACAAAGTTTGGCTTATTCATCATCACCAATATCTCAAGAGAAC 4242
Db 4198 CGGAGAGTTTTTGGCTACAAAGTTTGGCTTATTCATCATCACCAATATCTCAAGAGAAC 4257
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Db 4258 TGAAGCTGAGATTTGAATGGAGCTGCAGAAAGAAACAGCAACGCTGGAATCCGGAAG 4317
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Db 4318 TGCAGTATACATCTAATCATGCAAAATCTGCAACGTTGATTTCACTGAGCAACAATG 4377
Qy 4363 GACTTTATAGTACGCTTGCAGATTTGGCAACCGTTACTCAACCGTCCCTGTATATTC 4422
Db 4378 GACTTTATAGTACGCTTGCAGATTTGGCAACCGTTACTCAACCGTCCCTGTATATTC 4437
Qy 4423 GTGTTAATCAATTAACCGGTTAATTTGTTGATGATTTGAACCTTTGATCTGATTTA 4482
Db 4438 GTGTTAATCAATTAACCGGTTAATTTGTTGATGATTTGAACCTTTGATCTGATTTA 4497
Qy 4483 TCTTATCTGATCACCATTAAGCAACCGTTTACATTTACTGTTAGTTGGCGTGGCGA - 4540
Db 4498 TCTTATCTGATCACCATTAAGCTTACATTTACTGTTAGTTGGCGTGGCGA - 4556
Qy 4541 -----ATACCTAGTATGATGAGTTGCCACTCCCTATATGCGGC 4581
Db 4557 AAAGACTTACGATTCAGGCTTACCCCTAGTATGATGAGTTGGCACTCCCTCTGCGGCGC 4616
Qy 4582 TGCCTCGCTCGGTGGGCGCGGACAGAGAGCTTCCCGTCTGCGGACCTTTGTCGCA 4641
Db 4617 TGCCTCGCTCGGTGGGCGCGGACAGAGAGCTTCCCGTCTGCGGACCTTTGTCGCA 4676
Qy 4642 GGGCCACAGAGAGAGAGCGGATTTGAGAGAGTGGCCA 4683
Db 4677 GGGCCACAGAGAGAGAGCGGATTTGAGAGAGTGGCCA 4718

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QY	1783	GGGTGAGGCAACAACAGACCCGCCCGGATGACCGCGATTAAAGCAGCCCAAGCGGC	1842
Db	1789	GGGTGAGGCAACAAGACCCGCCCGGATGACCGCGATTAAAGCAGCCCAAGCGGC	1857
QY	1843	CTGCCCTCAGTCGGGGATCCATCGACGTCAGACGGGAGAGAGCTCCGGTGAATTTCG	1902
Db	1858	CTGCCCTCAGTCGGGGATCCATCGACGTCAGACGGGAGAGAGCTCCGGTGAATTTCG	1917
QY	1903	CGACAGGTACCAAAAACAATGTTCTGTCACGCGGGCAATGCTTCAGATGCTTTCCCTG	1962
Db	1918	CGACAGGTACCAAAAACAATGTTCTGTCACGCGGGCAATGCTTCAGATGCTTTCCCTG	1977
QY	1963	CAAAACATGCCAGAGATGATCAGAAATTTCAACTTTGCTTCACGCAACGGACCAAGA	2022
Db	1978	CAMGACATGCCAGAGATGATCAGAAATTTCAACTTTGCTTCACGCAACGGACCAAGA	2037
QY	2023	CTGTTCAAAATGTTTTCCCGCGGTCAGAAATCTCAACCGGTCGTCAAAAAGAGACTA	2082
Db	2038	CTGTTCAAAATGTTTTCCCGCGGTCAGAAATCTCAACCGGTCGTCAAAAAGAGACTA	2097
QY	2083	TCGAAAATCTGTGSCATTTCAATCTGCTGGGGGGGCTCCCGAGATTGCTTGCTCGG	2142
Db	2098	TCGAAAATCTGTGSCATTTCAATCTGCTGGGGGGGCTCCCGAGATTGCTTGCTCGG	2157
QY	2143	CTGCGATCTGGTCAACGTGGAATCTGGATGAATGTGTTTCTGAGCAATAATGACTTAA	2202
Db	2158	CTGCGATCTGGTCAACGTGGAATCTGGATGAATGTGTTTCTGAGCAATAATGACTTAA	2217
QY	2203	CAGGATATGGCTCCGATGTTTATCTTCCAGATTGGCTTGAGAGCAACCTCTCTGAGGCA	2262
Db	2218	CAGGATATGGCTCCGATGTTTATCTTCCAGATTGGCTTGAGAGCAACCTCTCTGAGGCA	2277
QY	2263	TTCCGCAATGGTGGGACTTGAACCTTGAGACCCCGAACCAGAAACCAACAGCAAAAAG	2322
Db	2278	TTCCGCAATGGTGGGACTTGAACCTTGAGACCCCGAACCAGAAACCAACAGCAAAAAG	2337
QY	2333	AGGACGACGGCCGGGCTGTGGTCTCTGCTCAACAGTACCTGGAACCTTCAACGGAC	2382
Db	2338	AGGACGACGGCCGGGCTGTGGTCTCTGCTCAACAGTACCTGGAACCTTCAACGGAC	2397
QY	2383	TCGACAAAGGGGAGCCCGTCAACGGGGGAGCGACGGCCCTCGAGACCAAGGCT	2442
Db	2398	TCGACAAAGGGGAGCCCGTCAACGGGGGAGCGACGGCCCTCGAGACCAAGGCT	2457
QY	2443	ACGACACAGAGCTCAAAAGCGGGTGCATCCGTATCTGCGGTATTAACAAGCGGACGGC	2502
Db	2458	ACGACACAGAGCTCAAAAGCGGGTGCATCCGTATCTGCGGTATTAACAAGCGGACGGC	2517
QY	2503	AGTTTCAGAGACGTTGTCNAAGATACGTCCTTTGGGGGCAACTCGGCGAGACAGCT	2562
Db	2518	AGTTTCAGAGACGTTGTCNAAGATACGTCCTTTGGGGGCAACTCGGCGAGACAGCT	2577
QY	2563	TCGAGGCCAAGAGAGGCTTCTCGAACCTTTTGCTCTGCTTGAGAAAGTCTAAAGCG	2622
Db	2578	TCGAGGCCAAGAGAGGCTTCTCGAACCTTTTGCTCTGCTTGAGAAAGGCTTAAAGCG	2637
QY	2633	CTCCTGAAAAAAGAAAGTCCGGTGAAGCACTGCGCAAGAGCCAGACTCTCTCTCGGCA	2682
Db	2638	CTCCTGAAAAAAGAAAGTCCGGTGAAGCACTGCGCAAGAGCCAGACTCTCTCTCGGCA	2697
QY	2683	TTGGCAAGACAGGCGCAGACCCGCTAAAAAGAGACTCAATTTTGGTCAAGTGGCACT	2742
Db	2698	TTGGCAAGACAGGCGCAGACCCGCTAAAAAGAGACTCAATTTTGGTCAAGTGGCACT	2757
QY	2743	CAGAGTCAGTCCCGGACCCACAACTCTCGGAGAACTTCAGCAACCCCGCTGCTGG	2802
Db	2758	CAGAGTCAGTCCCGGATCCCAACCTCTCGGAGAACTTCAGCAACCCCGCTGCTGG	2817
QY	2803	GACCTACTACATGGCTTCAGGCGGTGGCGCAACAAATGGCAGCAATTAAGAGAGCGCG	2862
Db	2818	GACCTACTACATGGCTTCAGGCGGTGGCGCAACAAATGGCAGCAATTAAGAGAGCGCG	2877
QY	2863	ACGAGTGGGTAAATGCTCAGAGAAATTGGCATTCAGATGCTGGGCAACAG	2922

Db	2878	ACGGAGTGGGTAAATCCTCAGGAAATTGGCAATTGGATTCCACATGCGTGGCGCAAG	2933
OY	2923	TCATACCAACCAAGCACCAGCAATGGGGCTTGGCCACCTATTAACAACACCTCTACAG	2982
Db	2938	TCATATCAACACAGCACCCGCACTGGGCTTGGCCCACTTACATTAACACCTTACAG	2997
OY	2983	AAATCTCAGTGTCTTCAACGGGGGGCAGCAACGACACCACTACTTGGCTTACAGACCC	3042
Db	2998	AAATCTCCAGTGTCTTCAACGGGGGGCAGCAACGACACCACTACTTGGCTTACAGACCC	3057
OY	3043	CTGGGGGGTATTTGATTTTCAACAGATTCCATGCAATTTCTACCAAGTGACTGGCAGC	3102
Db	3058	CTGGGGGGTATTTGATTTTCAACAGATTCTCATGCACTTTTTCACAGTGACTGGCAGC	3117
OY	3103	GACTATATCAACAATTTGGGGATTCCGGGCCAAGAGCTCAACTTAAGCTCTTCAACA	3162
Db	3118	GACTATATCAACAATTTGGGGATTCCGGGCCAAGAGCTCAACTTAAGCTCTTCAACA	3177
OY	3163	TCCAAGTCAAGAGAGTTCACGACGATGATGGCGTCAACACCATCGCTATATTAACCTT	3222
Db	3178	TCCAAGTCAAGAGAGTTCACGACGATGATGGCGTCAACACCATCGCTATATTAACCTT	3237
OY	3223	GCAAGGTTCAAGTCTTGTTCGGACTTCGAGTACCAAGTCCGTAAGCTCTGGCTTGGC	3282
Db	3238	GCAAGGTTCAAGTCTTGTTCGGACTTCGAGTACCAAGTCCGTAAGCTCTGGCTTGGC	3297
OY	3283	ACCAAGGCTGCTCCCTCCGCTCCGTTCCCGGGGACGTGTATATATTCGGAATACGGCTAC	3342
Db	3298	ACCAAGGCTGCTCCCTCCGCTCCGTTCCCGGGGACGTGTATATATTCGGAATACGGCTAC	3357
OY	3343	TAAAGCTCAAAATTTGGCAGCAGGCAAGTGGGACGCTCATCTTTTATCGCTGGAAATT	3402
Db	3358	TGACGCTCAAAATTTGGCAGCAGGCAAGTGGGACGCTCATCTTTTATCGCTGGAAATT	3417
OY	3403	TCCCATGCAATGCTGAGAAACGGGCAATTAATTCTTACCTTACAGCTACCTTCGAGAGC	3462
Db	3418	TCCCTTTCAGATGCTGAGAAACGGGCAATTAATTCTTACCTTACAGCTACCTTCGAGAG	3477
OY	3463	TGCCTTTTCAGAGAGCTACCGGCGCACAGCCAGAGCTGGACCGGCTGATGAACTCTCTCA	3522
Db	3478	TGCCTTTTCAGAGAGCTACCGGCGCACAGCCAGAGCTGGACCGGCTGATGAACTCTCTCA	3537
OY	3523	TCGACACAGTACTGATTAACCTGAAACAGAACTCAATCACTCCGGAAAGTACCCAAACA	3582
Db	3538	TCGACACATACCTGATTAACCTGAAACAGAACTCAATCACTCCGGAAAGTACCCAAACA	3597
OY	3583	AGGACTTGTCTTTAGCGTGGGTCTCAGCTGGCATGTCTGTTCAAGCCCAAAAACCTGGC	3642
Db	3598	AGGACTTGTCTTTAGCGTGGGTCTCAGCTGGCATGTCTGTTCAAGCCCAAAAACCTGGC	3657
OY	3643	TACCTGGAACCTGTTACCGGCGACAGAGCGGCTTTCTAATAACAAAACAGACAACAACA	3702
Db	3658	TACCTGGAACCTGTTATCGGCGACAGAGCGGCTTTCTAATAACAAAACAGACAACAACA	3717
OY	3703	GCAACTTATCACTGAGACTGTGTCTTCAAAATTAACCTTAATGGGCGTGAATCTATATCA	3762
Db	3718	GCAACTTATCACTGAGACTGTGTCTTCAAAATTAACCTTAATGGGCGTGAATCTATATCA	3777
OY	3763	ACCCTGGCACTGTATGGCTCACACAACAGACGACAAAGACAAAGTCTTTTCCATGAGCG	3822
Db	3778	ACCCTGGCACTGTATGGCTCACACAACAGACGACAAAGACAAAGTCTTTTCCATGAGCG	3837
OY	3823	GTCATCATGATTTTGGAAAGAGAGCGCCGAGCTTCAAAACATCTGACATTTGAACAATGTCA	3882
Db	3838	GTCATCATGATTTTGGAAAGAGAGCGCCGAGCTTCAAAACATCTGACATTTGAACAATGTCA	3897
OY	3883	TGATCATCAGACGAGAGGAAATCAAAAGCACTAACCCCGTGGCCACCGAAAGATTTTGGGA	3942
Db	3898	TGATTTACAGACGAGAGGAAATTAAGCCATTAACCTGTGGCCACCGAAAGATTTTGGGA	3957
OY	3943	CTGTGGCAGTCAATCTCCAGACGACGACAGACCTCTGGCACCGGAGATGTGCATTTTA	4002

Db	1018	CGGGGTGGTGGAGCCGGGGATCACTCCGAGGAAGATGGATCCAGAGAACAGAGC	1077
Oy	1063	CTCGAATCATCTCTTCAACAGCCGCTCCAACTCGGGGTCCAGATCAAGGCCGCTCTGGA	1122
Db	1078	CTCGAATCTCTTCAAGCCGCTTCCAACTCGGGGTCCAGATCAAGGCCGCTCTGGA	1137
Oy	1123	CAATGCCGGCAAGATCATGGCGCTGACCAAAATCCGGGCCGACTACCTTGTAAGGCCCGC	1182
Db	1138	CAATGCCGGCAAGATCATGGCGCTGACCAAAATCCGGGCCGACTACCTTGTAAGGCCCGC	1197
Oy	1183	TCGGCGCCGCAATTAACCAACCGCATTTACCGCATCTGTGAGCTGAACGGCTACGA	1242
Db	1198	TCGGCGCCGCAATTAACCAACCGCATTTACCGCATCTGTGAGCTGAACGGCTACGA	1257
Oy	1243	CCCTGCTACAGCCGGCTCGGTCTTCTCGGGCTGGGCCCAAGAAAAGTTTCGAAAAACGCA	1302
Db	1258	ACCTGCTACAGCCGGCTCGGTCTTCTCGGGCTGGGCCCAAGAAAAGTTTCGGAAGCCGA	1317
Oy	1303	CACCATCTGGCTGTTTGGAGCGGCCACCAACGGGCCAAGACCAACATCGCGAAGCCATCGC	1362
Db	1318	CACCATCTGGCTGTTTGGAGCGGCCACCAACGGGCCAAGACCAACATCGCGAAGCCATCGC	1377
Oy	1363	CCAGCGCGTGCCTTCTACAGCGCTGGCTCACTGACCAATGAAACTTTCCCTTCAACGA	1422
Db	1378	CCACGCGGTGCCTTCTACAGCGCTGGCTCACTGACCAATGAAACTTTCCCTTCAATGA	1437
Oy	1423	TTGGGTGCAACAAGATGTGATCTGGTGGGAGAGGCAAGATGACGGGCCAAGTCTGTGGA	1482
Db	1438	TTGGGTGCAACAAGATGTGATCTGGTGGGAGAGGCAAGATGACGGGCCAAGTCTGTGGA	1497
Oy	1483	GTCCGCAAGGCAATCTCTCGGCGSAGCAAGGTGTGGCTGTGACCAAAAGTCCAAAGTCTC	1542
Db	1498	GTCCGCAAGGCAATCTCTCGGCGSAGCAAGGTGTGGCTGTGACCAAAAGTCCAAAGTCTC	1557
Oy	1543	CGCCAGATCGATCCACCCCCGTGATGTCATCTTCAACAACCAACATGTGCGCCGTGAT	1602
Db	1558	CGCCAGATCGACCCCCCGGTGATGTCATCTTCAACAACCAACATGTGCGCGTAT	1617
Oy	1603	TGACGGGAAACAGCACCACTTTCAGACACACAGAGCCGTTTCAGAGACCGGATGTTCAATT	1662
Db	1618	TGACGGGAAACAGCACCACTTTCAGACACACAGAGCCGTTTCAGAGACCGGATGTTCAATT	1677
Oy	1663	TGAATCTACCCGCGCTGTGAGCATGACTTTGGSCAAAGGTGACAAAGCGAAGTCAAGA	1722
Db	1678	TGAATCTACCCGCGCTGTGAGCATGACTTTGGSCAAAGGTGAGCAAGCAAGTCAAGA	1737
Oy	1723	GTTCTTCCGCTGGGGGAGAGATCAGGTGACCGAGGTGGCGCATGAGTTCTACGTCAAAA	1782
Db	1738	GTTCTTCCGCTGGGGGAGAGATCAGGTGACCGAGGTGGCGCATGAGTTCTACGTCAAAA	1797
Oy	1783	GGGTGGAGACCAACACAGACCCCGCCCCGATGACCGCGGATTAAGAGGCCCAAGCGGGC	1842
Db	1798	GGGTGGAGACCAACCAAAAACCCGCCCCGATGACCGCGGATTAAGAGGCCCAAGCGGGC	1857
Oy	1843	CTGCCCTCAGTCCGGAGATCCATCGACGTCAGACGCGGAGAGGCTCCGCTGACCTTTCG	1902
Db	1858	CTGCCCTCAGTCCGGAGATCCATCGACGTCAGACGCGGAGAGGCTCCGCTGACCTTTCG	1917
Oy	1903	CGACAGGTACAAAACAATGTTCTCGTCAACGCGGSCATGCTTCAGATCTGTTCCTCG	1962
Db	1918	CGACAGGTACAAAACAATGTTCTCGTCAACGCGGSCATGCTTCAGATCTGTTCCTCG	1977
Oy	1963	CAAAAATGCCGAGAGATGAAATCAGAAATTTTCAACATTTTGCTTCAAGCACGGGACCAAGA	2022
Db	1978	CAAGCATGCGAGAAATGAATCAGAAATTTTCAACATTTTGCTTCAAGCACGGGACCAAGA	2037
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Db	2038	CTGTTCAAGATGTTTTCCCGGCGGTCTCAGAAATCTCAACCGGCTGTCAGAAAAGAGACGTA	2097
Oy	2083	TCGGAATCTGTGCAATTCATCATCTGCTGGGCGGGCTCCGAGATGTGTTGCTCGGC	2142

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Db	2158	CTGGCATCTGGTTCACAGCTGTGATCTGTGATCTGTGTTCTAGCAATTAATGACTTTAAAC	2217
Qy	2203	CAGGTATGGCTGCGGATGGTTATCTTCCAGATTGGCTTGAGAGCAACTCTCTGAGGSCA	2262
Db	2218	CAGGTATGGCTGCGGATGGTTATCTTCCAGATTGGCTTGAGAGCAACTCTCTGAGGSCA	2277
Qy	2263	TTTCGGCAGTGGTGGGACCTTGAACCTTGAGGCCGGAAACCCAAAGCCAAACAGCAAAAGC	2322
Db	2278	TTTCGGCAGTGGTGGGACCTTGAACCTTGAGGCCGGAAACCCAAAGCCAAACAGCAAAAGC	2333
Qy	2333	AGGACGACGGCGCGGGGCTGTGGTCTCTGTGCTACAGTACCTCGGACCTTTCACCGGAC	2382
Db	2338	AGGACGACGGCGCGGGGCTGTGGTCTCTGTGCTACAGTACCTCGGACCTTTCACCGGAC	2397
Qy	2393	TCGACAAAGGGGAGAGCCCGTCAACCGCGCGGATGCAAGCGGCCCTTGAGCAACAAGGCT	2442
Db	2398	TCGACAAAGGGGAGAGCCCGTCAACCGCGCGGATGCAAGCGGCCCTTGAGCAACAAGGCT	2455
Qy	2443	ACGACACGACACTCAAAGCGGCTGACATCTCGTACTCGCGGTATATACACGCGGACGCG	2502
Db	2458	ACGACACGACACTCAAAGCGGCTGACATCTCGTACTCGCGGTATATACACGCGGACGCG	2517
Qy	2503	AGTTTCAGGACGCTGTGCAAGAAGTACGTCTTTTGGGGGGCAACTCGGCGGAGCAAGCT	2562
Db	2518	AGTTTCAGGACGCTGTGCAAGAAGTACGTCTTTTGGGGGGCAACTCGGCGGAGCAAGCT	2577
Qy	2563	TCGAGGCCAAGAAGGGTTCTCGAACCCTTTTGGTCTGTGTGAGGAAGTGTCTAAGACGG	2622
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Qy	2803	GACCTACTCAATGGCTTCAGGCGGTGGCGCAACATGGCAGACATTAACGAGGCGCGC	2862
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Qy	3043	CTGGGGGATTTTGGATTTCACAGATTCACCTGCACTTTTTCACACAGTACCTGGGACG	3102
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Qy	3103	GACTCATCAACAATTTGGGATTTCCGGGCCCAAGAGACTCAACTCAAGCTCTTCAACA	3162
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Qy	3163	TCGAAATCAGGAGGTCAAGCAATGATGGCGTCAAGACCATGCTTAATTAACCTTACCA	3222
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; Publication No. US20030138772A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (f
; FILE REFERENCE: UBN-02735USA
; CURRENT APPLICATION NUMBER: US/10/291,583
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/350,607
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/341,117
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/377,066
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/386,675
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4721
; TYPE: DNA
; ORGANISM: adeno-associated virus serotype 7
US-10-291-583-1

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Query Match 78.5%; Score 3678.4; DB 7; Length 4721;
Best Local Similarity 87.5%; Pred. No. 0;
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Db 2638 TCTTGGAAAGAAAGACCGGTAGAGCAGTCCGCAAGGTTCCCGGACTCTCCAGCGG 2697
Qy 2661 CATTGGCAAGAGAGCCAGAGCCCGCTTAAAAAGACTCAATTTTGGTCAAGCTGGCGA 2740
Db 2698 CATCGGCAAGAAAGGCGAGAGCCCGCAAGAAAGAGACTCAATTTTGGTCAAGCTGGCGA 2757
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Db 2758 CTCAGAGTCAAGTCCCGGACCCCAACACTCTGGAGAACCTTCAGAGAACCCCGCTGGCTGT 2817
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Qy 3161 CATCCAACTCAAGAGGTCAAGCAATGATGCGTCAAGCAACATCGCTAAATTAACCTTAC 3220
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OY	453 8	CGA-----	ATACCCCTAGTATGAGATTGCCCATCTCCCTCAT	457 5
Db	455 4	CGAATPAGAACACTGACGTACACCGCGTACCCCTATGTATGAGATTGGCAGCTCCCTCAT		461 3
OY	457 6	GGCGCGCTGCCTCGCTCGGTGGGGGCGGAGAGAGAGCTCTGCGGTCTGGCGAGACTTTGG		465 5
Db	461 4	GGCGCGCTGCCTCGCTCGGTGGGGGCGTGGAGACCAAGGTCCGCAACGCGAGAGCTCTGC		467 3
OY	463 6	TCCGCGAGGCCCAACCGAGCGAGCGAGCGCATAGAGGAGTGGCCAA	468 3	
Db	467 4	TCTGCGGCGCCCAACGAGCGAGCGAGCGCGCATAGAGGAGTGGCCAA	472 1	

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RESULT 15
US-11-145-035-37
; Sequence 37, Application US/11145035
; Publication NO. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145, 035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 4721
; TYPE: DNA
; ORGANISM: Adeno-associated virus 7
US-11-145-035-37

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Query Match	78.5%	Score 3678.4	DB 15	Length 4721
Best Local Similarity	87.5%	Pred. No. 0		
Matches 4135	Conservative	0	Mismatches 541	Indels 52
				Gaps 8

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Db	1	TTGGCACTCCCTCTCTGCGGGGCTCGCTCGCTCGATGGGGGCTCGCGACCAAGTCGCC	60
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Db	61	AGACGGCAGAGCTCTGCTCTGCGGGCCCAACGAGCGAGCGAGCGCATGAGAGTG	120
OY	121	GGCAATCCCATCTAAGGGTTCTTGAGG-----GTTGAGTCTGTAC	164
Db	121	GGCAATCCCATCTAAGGGTTACCGCAAGGCGCTCCACGCTCCCGCTGAGGCTGAC	180
OY	165	GTGAATTACGTCATAGGGTTAGGAGGTCCTGTATTAGAGTCACTGAGTG--TTTGGC	223
Db	181	GTAAATCACTGCATAGGG---GATGGTCCGTATTAGCTGTCACTGAGTGCCTTTGGC	237
OY	224	ACATTTTGGCAGACCAATGTGTCACTCGGTATTTAAGCCCGATGACACGAGGTC	283
Db	238	ACATTTTGGCAGACCACTGTGCTCTTTGAGGTATATATGCGCGATGACGACGAGATC	297
OY	284	TCCATTTTGAAGCGGAGTTTGAACGCGCGAGCGGCGGAGTTTACGATTGTG	343
Db	298	TCCATTTTGAACCGGAAATTGAAACGAGCAGCAGCAGCAGTCCGGGTTCTACAGATCTG	357
OY	344	ATTAAAGTCCCGACGACCTTGAAGAGCATTGCCTCGGACATTTTGAACGCTTTGTAAC	403
Db	358	ATCAAGGTGCGAGACGACTGAGAGAGCACTGCGGGCATTCTGTGACTGTTGTGAAC	417
OY	404	TGGGTGGCCGAGAGGATGGGAGTTTGGCCGACATTTGACATGAGATCTGAATCTGATT	463
Db	418	TGGGTGGCCGAGAGGATGGGAGTCTGCCCGGATTTGACATGAGATCTGAATCTGATC	477
OY	464	GAGCAGCACTCTGACCTGGGCGGAGAACTGACAGCGCATTTCTGTTCCATGTGCGC	523

Db	478	GAGCAGGACCCCTCAACCGTGGCCGAGAACTGCAACCGCATTTCTTGSTCCAAATGGCC	537
Qy	524	CGCGTAGTAAGGCCCGGAGGCGCTCTTCTTTGTTCAAGTTGAGAAAGGCGAGTCTTAAC	583
Db	538	CGCGTAGTAAGGCCCGGAGGCGCTGTCTTTGTTCAAGTTGAGAAAGGCGAGACTAAC	597
Qy	584	TTCCACCTTCATATTTCTGTGGAGACCAACGGGGGTTCAATCCATGCTGTGGGCGCTTC	643
Db	598	TTCCACCTTCACGTTCTGTGTGGAGACCAACGGGGGTTCAATCCATGCTGTAGGCGCTTC	657
Qy	644	CTGAGTCAAGATTAGCGAACAGCTGGTGGAGCAATCTACCGGGGATGAGCGCACCGTG	703
Db	658	CTGAGTCAAGATTCGGGAAGAGCTGATCCAGACCATCTACCGGGGGTGGAGCCACGCTG	717
Qy	704	CCCAACTGGTTCCGCGTGACCAAGACGCGTATGCGCGCGAGGGGGAAACAAGTGTG	763
Db	718	CCCAACTGGTTCCGCGTGACCAAGACGCGTATGCGCGCGGGGGGAAACAAGTGTG	777
Qy	764	GACGAGTCTACATCCCAACTACCTCTGCGCCCAAGACTCAAGCCGAGCTGCATGGGCG	823
Db	778	GACGAGTCTACATCCCAACTACCTCTGCGCCCAAGACCAGCCGAGCTGCATGGGCG	837
Qy	824	TGCAATTACATGAGAGAGTATATTAAGCGCGTTTAAACCTGGCCGAGCCGAAAGGGCTC	883
Db	838	TGCAATTACATGAGAGAGTATATTAAGCGCGTTTGAACTGGCCGAAACGAAAGGGCTC	897
Qy	884	GTGGCGCAGACCTTACCCACGTCAGCCAGAACCCAGAGACGAAACAAGAGATCTGAAC	943
Db	898	GTGGCGCAGACCTTACCCACGTCAGCCAGAACCGAGAGCAGAACAGAGAAATTGAAC	957
Qy	944	CCCAATTTCTGACGCGCTGTATCCGATCCGATCAAAAACTTCGCAACGCTACATGAGCTG	1003
Db	958	CCCAATTTCTGACGCGCGCTGTATCCGATCCGATCAAAAACTTCGCGCTACATGAGCTG	1017
Qy	1004	GGGTGGCTGTGTGACCGGGGTCATCACTTCGAGAAAGCATGTGATCCAGAGACCAAGCC	1066
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Db	1078	TGATCATCTCTTTCAACGCGCGCTCAACTCGCGGTCCCAAGATCAAGGCGCGCTGTGAC	1133
Qy	1124	AATGCGGCAAGATCATGCGCTGACCAATTCGCGCCGACTACCTGTAGGCCCGCT	1183
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Qy	1184	CGGCGCGCGCAATTAAAACCAACCGCATTTTACCGCATCTGTGAGCTGAACGGCTACGAC	1244
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Qy	1364	CACGCGGTGCCCTTCTACGCGCTGCGTCAACTGACCAATGAGAACTTTCCCTTCAACGAT	1423
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Dh 1618 GACGGGAACAGCACCACTTTGAGCAACAGAGCCGTTGAGAACCGGAATGTTCAATT 1677
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Dh 1858 TGCCCTCAGTCGCGGATCCATCGACGTCAGACCGGAGAGGCTCCGCTGACCTTTGCC 1917
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DB 4674 TCTGCGGCGCCACCGAGCGAGCGGCACTAAGAGGAGTGGCCAA 4721

Search completed: June 13, 2006, 14:01:45
Job time : 3606 secs

THE FREE BLANK (USPTO)

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 12:58:58 ; Search time 843 Seconds
(without alignments) 10394.309 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4683	100.0	4683	US-09-807-802A-19	Sequence 19, Appl1
2	4253.2	90.8	4718	US-09-807-802A-1	Sequence 1, Appl1
3	3296.2	70.4	4679	US-10-038-972A-12	Sequence 12, Appl1
4	3296.2	70.4	8698	US-09-770-315-2	Sequence 2, Appl1
5	3293	70.3	4679	US-09-717-789C-25	Sequence 25, Appl1
6	3270.8	69.8	4680	US-08-254-358-1	Sequence 1, Appl1
7	3270.8	69.8	4680	US-08-475-391-1	Sequence 1, Appl1
8	3270.8	69.8	4680	US-08-709-609-1	Sequence 1, Appl1
9	3270.8	69.8	4680	PCT-US95-07178-1	Sequence 1, Appl1
10	3267.8	69.8	4681	US-09-807-802A-18	Sequence 18, Appl1
11	3244.2	69.3	4675	US-09-783-378A-1	Sequence 1, Appl1
12	3244.2	69.3	4675	US-09-783-378A-2	Sequence 2, Appl1
13	3244.2	69.3	4675	US-10-111-708-1	Sequence 1, Appl1
14	3114.4	66.5	7557	US-09-770-315-3	Sequence 3, Appl1
15	3008	64.2	8159	US-09-438-268-5	Sequence 5, Appl1
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17	2532	54.1	4767	US-09-533-594B-1	Sequence 1, Appl1
18	2504.4	53.5	7214	US-09-438-268-1	Sequence 1, Appl1
19	2103.8	44.9	2211	US-09-807-802A-12	Sequence 12, Appl1
20	2097.4	44.8	7447	US-10-216-870-11	Sequence 11, Appl1
21	1812.8	38.7	1872	US-09-807-802A-4	Sequence 4, Appl1
22	1715.2	36.6	4072	US-09-770-315-4	Sequence 4, Appl1
23	1705.6	36.4	1800	US-09-807-802A-14	Sequence 14, Appl1

24	1540.8	32.9	1641	US-09-807-802A-6	Sequence 6, Appl1
25	1513.8	32.3	1605	US-09-807-802A-16	Sequence 16, Appl1
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37	935.6	20.0	2208	US-09-533-594B-5	Sequence 5, Appl1
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ALIGNMENTS

RESULT 1
US-09-807-802A-19
Sequence 19, Appl1 Application US/09807802A

Patent No. 6759237

GENERAL INFORMATION:

APPLICANT: Wilson, James M.

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,

FILE REFERENCE: GNPVN.031USA

CURRENT APPLICATION NUMBER: US/09/807, 802A.

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107, 114

PRIOR FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 4683

TYPE: DNA

ORGANISM: AAY-6

US-09-807-802A-19

Query Match 100.0%; Score 4683; DB 3; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	3661	GGCAGCAGCGCGTTTCTAAAACAAAAAAGACACACAAACAGCAACTTTACTGGAAGT	3720
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RESULT 2			
US-09-807-802A-1			
; Sequence 1, Application US/09807802A			
; Patent No. 6759237			
; GENERAL INFORMATION:			
; APPLICANT: Wilson, James M.			
; APPLICANT: Xiao, Weidong			
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences			
; TITLE OF INVENTION: Vectors and Host Cells Containing Same			
; FILE REFERENCE: GNPVN.031USA			
; CURRENT APPLICATION NUMBER: US/09/807, 802A			
; PRIOR FILING DATE: 2002-02-21			
; PRIOR APPLICATION NUMBER: US 60/107,114			
; PRIOR FILING DATE: 1998-11-05			
; PRIOR APPLICATION NUMBER: PCT/US99/25694			
; PRIOR FILING DATE: 1999-11-02			
; NUMBER OF SEQ ID NOS: 20			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 4718			
; TYPE: DNA			
; ORGANISM: AAV-1			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (335)..(2206)			
; OTHER INFORMATION:			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (2223)..(4430)			
; OTHER INFORMATION:			
US-09-807-802A-1			
Query Match			
Best Local Similarity 90.8%; Score 4253.2; DB 3; Length 4718;			
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;			
QY	1	TTGGCCACTCCCTCTTGCSCGCTCGCTCACTAGGCGGGCGACCAAAAGTGGCC	60
Db	1	TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCGGTGGGGCTGCGAACAAAGTTCGC	60
QY	61	CGAGCGCCGGGCTTGGCCCGGGCGGCGCTCAGTGAAGGAGGAGCGGCAGAGAGGAGTG	120
Db	61	AGAAGGCGAGAGCTCTGCTCTCCGGCCCGACCGAGCGAGCGCGCAAGAGAGGAGTG	120
QY	121	GCCAATCTCATCACTAGAGGGT-----TCCTGAGAGGAGTGAAGTCGTGA	163
Db	121	GGAACCTCATCACTAGAGGGTAATCGAGAGCGCCTCCACAGCTGCGCGTCAAGCGCTGA	180
QY	164	CGTGAATTACGTCATAGGGGTTAAGGAGGTCTGTATTAGAGTCAAGTGAAGT- TTTTGC	222
Db	181	CGTAATAATGATCAATAGG---GAGTGGTCTGTATTAGCTGATCAAGTGAAGTCTTTTGC	237
QY	223	GACATTTTGGACACCAATGTGTACAGCTGGGATTTTAAAGCCCGAGTGAACACAGAGGT	282
Db	238	GACATTTTGGACACACAGCTGGCCATTTAAGGTTATATATGGCCGAGTGAAGCGAGAGAT	297
QY	283	CTCCATTTTGAAGCGGAGGATTTGAAGCGCGACGCGCATGCGGGGTTTAAACAGATTGT	342
Db	298	CTCCATTTTGAACCGGAAATTTGAACGAGCAAGCATGCGGGCTTTTACAGAGATCGT	357
QY	343	GATTAAAGGTCCCGACCGAATTGAAGAGCATCTAGCCCGGCAATTTCTGACAGCTTTGGAA	402
Db	358	GATCAAGGTGCGAGCGAATCTGAGAGACATCTGCCGGGCAATTTCTAATCGTTTGGAG	417
QY	403	CTGGGTGGCGGAGAGGAATGGAGTTGGCGCCAGATTTCTGACATGAGATCTGAATCTGAT	462

Db	418	CTGGGTGGCCGAGAAAGAAATGGAGACTGCCCCCGGATTTGACATGATCTGAAATCGAT	4177
Qy	463	TGAGCAGGCACCCCTTGACCGTGGCCGAGAAAGCTGCAAGCCGACCTTCTTGATCCATGAGCG	522
Db	478	TGACACAGGCACCCCTTGACCGTGGCCGAGAAAGCTGCAAGCCGACCTTCTTGATCCATGAGCG	537
Qy	523	CCGGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTGTGTCAAGTTCAGAAAGGAGCGAGTCTTA	582
Db	538	CCGGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTGTGTCAAGTTCAGAAAGGAGCGAGTCTTA	597
Qy	583	CTTCCACCTCCATATTCTGTGTGAGACCAACGAGGGGTCAAAATCAATGCTGTGGCCGCTT	642
Db	598	CTTCCACCTCCATATTCTGTGTGAGACCAACGAGGGGTCAAAATCAATGCTGTGGCCGCTT	657
Qy	643	CCTGATGCAGATTATGGCACAAGCTGGTGGAGACCATCTACCGGGGAGTGGAGCCGACCCCT	702
Db	658	CCTGATGCAGATTATGGCACAAGCTGGTGGAGACCATCTACCGGGGAGTGGAGCCGACCCCT	717
Qy	703	GCCCCACTGGTTCACGGTGAACCAAGACGCGTAAATGGCCGCGAGGGGGGAAACAAGTGAT	762
Db	718	GCCCCACTGGTTCACGGTGAACCAAGACGCGTAAATGGCCGCGAGGGGGGAAACAAGTGAT	777
Qy	763	GGAGAGTGCCTACATCCCAACTCTCTCTGCCCCAAGCTCAAGCCCGAGCTGCAAGTGGCG	822
Db	778	GGAGAGTGCCTACATCCCAACTCTCTCTGCCCCAAGCTCAAGCCCGAGCTGCAAGTGGCG	837
Qy	823	GTGACCTAACATGAGAGAGTATATTAACGCGGTGTTTAAACTTGAGCCGACGCAAAACGACT	882
Db	838	GTGACCTAACATGAGAGAGTATATTAACGCGGTGTTTAAACTTGAGCCGACGCAAAACGACT	897
Qy	883	CGTGGCGCAGACCTTGACCCACGTCGACGACAGCCAGAGACAGAACAAAGAAATCTGA	942
Db	898	CGTGGCGCAGACCTTGACCCACGTCGACGACAGCCAGAGACAGAACAAAGAAATCTGA	957
Qy	943	CCCCAATTCTACGCGCGCTGTCAATCCGGTCAAAAACCTCCGACCGCTACATGAGAGCTGT	1002
Db	958	CCCCAATTCTACGCGCGCTGTCAATCCGGTCAAAAACCTCCGCGGCTACATGAGAGCTGT	1017
Qy	1003	CGGGTGGCTGTGAGACCGGGGCATCACCTCCGAGAACAGTGAATCCAGAGAGACCAAGCC	1062
Db	1018	CGGGTGGCTGTGAGACCGGGGCATCACCTCCGAGAACAGTGAATCCAGAGAGACCAAGCC	1077
Qy	1063	CTCGATCACTCTCTTCAACCGCGGCTCAACTCGGGTCCCAAGTCAAAAGCCGCTCGA	1122
Db	1078	CTCGATCACTCTCTTCAACCGCGGCTCAACTCGGGTCCCAAGTCAAAAGCCGCTCGA	1137
Qy	1123	CAATGCCGCGAAGATCAATGAGCGCTGACCAAAATCCGCGCCGACCTACTGTAGGCCCGC	1182
Db	1138	CAATGCCGCGAAGATCAATGAGCGCTGACCAAAATCCGCGCCGACCTACTGTAGGCCCGC	1197
Qy	1183	TCCGCCGCGCAGCATTTAAACCAACCGCATTTATCCGCATCTGTGAGCTGAACGGCTTACGA	1242
Db	1198	TCCGCCGCGCAGCATTTAAACCAACCGCATTTATCCGCATCTGTGAGCTGAACGGCTTACGA	1257
Qy	1243	CCCGTCCAGACCGGCTCCGCTCTTCTTCGAGCTGGGCCCAAGAAAAGTTCGAGAAAACGCA	1302
Db	1258	ACCTGCTCAACCGGCTCCGCTCTTCTTCGAGCTGGGCCCAAGAAAAGTTCGAGAAAACGCA	1317
Qy	1303	CACCATCTGAGTGTGGGCCGACCAACGAGGCAAGACCAACATCGCGAAGCCATCGC	1362
Db	1318	CACCATCTGAGTGTGGGCCGACCAACGAGGCAAGACCAACATCGCGAAGCCATCGC	1377
Qy	1363	CCAGGCGGTGCCCTTCAACGGCTGCGGTCACTGGACCAATGAGAACTTCCCTTCAACGA	1422
Db	1378	CCAGGCGGTGCCCTTCAACGGCTGCGGTCACTGGACCAATGAGAACTTCCCTTCAATGA	1437
Qy	1423	TTGCGTCCAGCAAGATGATCTGTGTGAGAGAGGCGCAAGATGACCGCCAAAGTCTGTGA	1482
Db	1438	TTGCGTCCAGCAAGATGATCTGTGTGAGAGAGGCGCAAGATGACCGCCAAAGTCTGTGA	1497
Qy	1483	GTCCGCCAAGGCATTTCTCGGCGGACAGAGTGCCTGTGAACCAAAAGTTCAGAGTGTCTC	1542
Db	1498	GTCCGCCAAGGCATTTCTCGGCGGACAGAGTGCCTGTGAACCAAAAGTTCAGAGTGTCTC	1557

OY	1543	CGCCCAAGTCCATCCCAACCCCGGTATGTGCACTCTCAACCAACATATGCGCCGTAT	1602
Db	1558	CGCCCAAGTCCAGCCCAACCCCGCGTATGTCACTCTCAACCAACATATGCGCCGTAT	1617
OY	1603	TGACGGGAACAGCAACCACTTCTGAGACACAGAGCGGTGCGAGCCGGATGTTCAATT	1662
Db	1618	TGACGGGAACAGCAACCACTTCTGAGACACAGAGCGGTGCGAGCCGGATGTTCAATT	1677
OY	1663	TGAATTCAACCCGCGCTCTGAGCATGACTTTGGCAAGGTGACCAAGCAGAAAGTCAAGA	1722
Db	1678	TGAATTCAACCCGCGCTCTGAGCATGACTTTGGCAAGGTGACCAAGCAGAAAGTCAAGA	1737
OY	1723	GTTCTTCGGCTGGGGGCGAGGATCAGGTACCGAGGTGCGCATGAGTCTTAAGTCAGAAA	1782
Db	1738	GTTCTTCGGCTGGGGGCGAGGATCAGGTACCGAGGTGCGCATGAGTCTTAAGTCAGAAA	1797
OY	1783	GGGTGGAGCCAAACAAGCCCCCGCTCGATGACCGCGATTAAGCGAGCCCAAGCGGC	1842
Db	1798	GGGTGGAGCCAAACAAGCCCCCGCTCGATGACCGCGATTAAGCGAGCCCAAGCGGC	1857
OY	1843	CTGCCCCCTCAGTCTGGGGATCCATCGACGTCAAGCCGGGAAGAGCTCCGGTGAATTGGC	1902
Db	1858	CTGCCCCCTCAGTCTGGGGATCCATCGACGTCAAGCCGGGAAGAGCTCCGGTGAATTGGC	1917
OY	1903	CGACAGGTACCAAAACAATGTTCTCTGCAAGCGGGGCAATGCTTGAGTGTCTTCCCTG	1962
Db	1918	CGACAGGTACCAAAACAATGTTCTCTGCAAGCGGGGCAATGCTTGAGTGTCTTCCCTG	1977
OY	1963	CAAAACATGCGAGAGATGAAATCAGAAATTTCAACTTTTGCTTCAACGACGGGAACGAGA	2022
Db	1978	CAAGCAGATGCGAGAGATGAAATCAGAAATTTCAACTTTTGCTTCAACGCGGAGCAGAGGA	2037
OY	2023	CTGTTCAAGATGTTCCCGCGCGTGCAGATCTTCAACCGGTCGTCAAGAAAGAGAGCTA	2082
Db	2038	CTGTTCAAGATGCTTCCCGCGGCTCAAGATCTTCAACCGGTCGTCAAGAAAGAGAGCTA	2097
OY	2083	TCGGAACTCTGTGCAATTCATCTGCTGAGGCGGCTCCCGAGATTGCTTCTCGGC	2142
Db	2098	TCGGAACTCTGTGCAATTCATCTGCTGAGGCGGCTCCCGAGATTGCTTCTCGGC	2157
OY	2143	CTGCGATCTGGTCAACGTGGAATCTGGATGACTGTGTTCTGAGCAATAATGACTTAAAC	2202
Db	2158	CTGCGATCTGGTCAACGTGGAATCTGGATGACTGTGTTCTGAGCAATAATGACTTAAAC	2217
OY	2203	CAGGTAATGGCTGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACCTCTGAGGGCA	2262
Db	2218	CAGGTAATGGCTGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACCTCTCTGAGGGCA	2277
OY	2263	TTCCGACATGTTGGACTTTGAACCTGTGAGCCCCGAAACCCAAAGCCAACGACGAAAGC	2322
Db	2278	TTCCGACATGTTGGGACTTTGAACCTGTGAGCCCCGAAAGCCAAAGCCAACGACGAAAGC	2337
OY	2323	AGGACGAAGGCGGGGTCTGGTGTCTCTGCTCAAGTACTCGGACCTTCAACCGAC	2382
Db	2338	AGGACGAAGGCGGGGTCTGGTGTCTCTGCTCAAGTACTCGGACCTTCAACCGAC	2397
OY	2383	TCGACAAAGGGGAGGCCGTCAACGCGGCGGATGAGCGGCGCTCGAGCACGACGAGCT	2442
Db	2398	TCGACAAAGGGGAGGCCGTCAACGCGGCGGATGAGCGGCGCTCGAGCACGACGAGCT	2457
OY	2443	ACGACCAAGCACTCAAAAGCGGTGACAATCTGTAACCTGCGGTATACACGCGCAGCGCG	2502
Db	2458	ACGACCAAGCACTCAAAAGCGGTGACAATCTGTAACCTGCGGTATACACGCGCAGCGCG	2517
OY	2503	AGTTTCAGAGACGTCTGCAAGAAGTACGTCTTTTGGGGGCAACTCTGGGGAGACAGTCT	2562
Db	2518	AGTTTCAGAGACGTCTGCAAGAAGTACGTCTTTTGGGGGCAACTCTGGGGAGACAGTCT	2577
OY	2563	TCGAGGCCAAGAAGAGGTTCTCGAACCCTTTTGGTCTGCTTGAGAGAGTCTTAAGCAG	2622
Db	2578	TCGAGGCCAAGAAGAGGTTCTCTGCAACCTCTCGCTCTGTTGAGAGAGGCTTAAGCAG	2637

QY	2632	CTCCGAGAAAGAAACGTCOCGGTAAGAGCAGTGCCTCAAGAGCAGACCTCCTCCGGGCA	2682
Db	2638	CTCTCGAGAAAGAAAGTCGGTAGAGCAGTGCCTCAAGAGCAGACCTCCTCCGGGCA	2697
QY	2683	TTGGCAAGACAGAGCCAGCAGCCCGCTAAAGAGACTCAATTTTGGTCAGACTGGCGACT	2742
Db	2698	TCGGCAAGACAGGCCAGCAGCCCGCTAAAGAGACTCAATTTTGGTCAGACTGGCGACT	2757
QY	2743	CAGAGTCAGTCCCGGACCCGACACCTCTCCGAGAACTTCGAGCAACCCCGCTGCTGG	2802
Db	2758	CAGAGTCAGTCCCGGATCCACAACTCTCCGAGAACTTCGAGCAACCCCGCTGCTGG	2817
QY	2803	GACCTACTACAAATGGCTTCAGGCGGTGGCGCAACCAATGGCAGACAAATAAGAGCGCGCG	2862
Db	2818	GACCTACTACAAATGGCTTCAGGCGGTGGCGCAACCAATGGCAGACAAATAAGAGCGCGCG	2877
QY	2863	ACGGAGTGGGTATATGCTCAGAGAAATTGGCAATTCCACATGGCTGGGCGCAGAG	2922
Db	2878	ACGGAGTGGGTATATGCTCAGAGAAATTGGCAATTCCACATGGCTGGGCGCAGAG	2933
QY	2923	TCATCACCACCGACCCGAACTGGGCTTGGCCACTATACAAACCACTCTACAAAGC	2982
Db	2938	TCATCACCACCGACCCGACCTGGGCTTGGCCACTATACAAATACCACTCTACAAAGC	2997
QY	2983	AAATCTCAGTGTCTTCAACGGGGGCGAGCAACGACACCACTACTCCGCTACAGACCC	3042
Db	2998	AAATCTCAGTGTCTTCAACGGGGGCGAGCAACGACACCACTACTCCGCTACAGACCC	3057
QY	3043	CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCACTTCCACACAGTACCTGGAGC	3102
Db	3058	CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCACTTTCACACAGTACCTGGAGC	3117
QY	3103	GACTCATCAACAAACAATTGGGGATTCCGGCCCAAGAGACTCACTTCAAGCTCTTCAACA	3162
Db	3118	GACTCATCAACAAACAATTGGGGATTCCGGCCCAAGAGACTCACTTCAACACTCTTCAACA	3177
QY	3163	TCCAAGTCAGAGAGGTACGACGAAATGATGGCGTCAAGCAATGCTATATACTTACCA	3222
Db	3178	TCCAAGTCAGAGAGGTACGACGAAATGATGGCGTCAACAACATGCTATATACTTACCA	3237
QY	3223	GCAGGGTTCAAGTCTTGTCCGACTCCGAGTACAGTTCCCGTATAGTCTCGGCTCTGGCG	3282
Db	3238	GCAGGGTTCAAGTCTTGTCCGACTCCGAGTACAGTTCCCGTATAGTCTCGGCTCTGGCG	3297
QY	3283	ACCAAGGCTGCTCCCTCCGTTCCCGGCGAGCGTTCAATATTCGCGAGTACGGCTAC	3342
Db	3298	ACCAAGGCTGCTCCCTCCGTTCCCGGCGAGCGTTCAATATTCGCGAGTACGGCTAC	3357
QY	3343	TAAAGCTCAACAATGGCAGCCAGGCAAGTGGGACGCTCACTCTTACTGCTGGAAATTT	3402
Db	3358	TAAAGCTCAACAATGGCAGCCAGGCAAGTGGGACGCTCACTCTTACTGCTGGAAATTT	3417
QY	3403	TCCCATCGCAGATGCTGAGAAACGGGCAATTAATTACTCTTACGTAACCTTCGAGAGC	3462
Db	3418	TCCCATCGCAGATGCTGAGAAACGGGCAATTAATTACTCTTACGTAACCTTCGAGAGC	3477
QY	3463	TGCGTTTTCACAGAGCTACGCGCAGCCAGACCTGGAGCCGGCTGATGATCCTCTTCA	3537
Db	3523	TGCGTTTTCACAGAGCTACGCGCAGCCAGACCTGGAGCCGGCTGATGATCCTCTTCA	3582
QY	3528	TCGACCAATACCTGTATTACTGTAACGAAATCTCAAAATACGTCCGGAAGTCCCAAAACA	3597
Db	3583	TCGACCAATACCTGTATTACTGTAACGAAATCTCAAAATACGTCCGGAAGTCCCAAAACA	3642
QY	3598	AGGACTTGGCTGTATTAAGCCGTGGGCTCTCAGCTGGCAATGCTGTTCACGCCCAAAACCTGGC	3657
Db	3643	TACCTGGACCTGTATTAAGCCGTGGGCTCTTAAACCAAAACAGACAAACAACA	3702
QY	3658	TACCTGGACCTGTATTAAGCCGTGGGCTCTTAAACCAAAACAGACAAACAACA	3717
QY	3703	GCAACTTATACCTGAGCTGTGCTTCAAAATATTAACCTTAATGGCGCTGAATCTATATCA	3762

Db 3718 GCAATTTTACCTGGACCTGGCTCTTCAAAATATACTCAATGGGGTAACTCAATCA 3777
Qy 3763 ACCCTGGACCTGTAATGGCTTCAACAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3822
Db 3778 ACCCTGGACCTGTAATGGCTTCAACAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3837
Qy 3823 GTGTCAATATTTTGGAAAGAGAGCGCGGAGCTTCAACACATGCTATTGGACATGTCA 3882
Db 3838 GTGTCAATATTTTGGAAAGAGAGCGCGGAGCTTCAACACATGCTATTGGACATGTCA 3897
Qy 3883 TGATCAACAGAGAGAGAGAAATCAAAAGCCACTAAACCCCTGGCCACCGAAAGATTGGGA 3942
Db 3898 TGATTAACAGAGAGAGAGAAATTAAGCCACTAAACCCCTGGCCACCGAAAGATTGGGA 3957
Qy 3943 CTGTGGCAGTCAATCTCCAGAGCAGACAGACACCTTGGACCGGAGATGTGATGTA 4002
Db 3958 CCGTGGCAGTCAATTTTCCAGAGCAGACAGACACCTTGGACCGGAGATGTGATGTA 4017
Qy 4003 TGGGAGCTTACCTGGAATGGTGTGGCAAGA CAGAGAGTATACCTGAGGGGCTTATTT 4062
Db 4018 TGGGAGCTTACCTGGAATGGTGTGGCAAGATAGAGAGTGTACTGAGGGGCTTATTT 4077
Qy 4063 GGGCCAAAATTCCTCAACGAGATGGA CATTTCACCCGCTCTCTTCATGGGCGGCTTTG 4122
Db 4078 GGGCCAAAATTCCTCAACAGATGGA CATTTCACCCGCTCTCTTCATGGGCGGCTTTG 4137
Qy 4123 GACTTAAGCACCCTGCTCTCAATCTCAATCAAAACAGACCTGTTCTTCTGCAATCTC 4182
Db 4138 GACTTAAGAACCCCTGCTCTCAATCTCAATCAAAACAGACCTGTTCTTCTGCAATCTC 4197
Qy 4183 CGGAGAGTTTTCGGCTCAAAAGTTTGGCTTATTCATCAACCAAGATTCACAGAGACAG 4242
Db 4198 CGGAGAGTTTTCGGCTCAAAAGTTTGGCTTATTCATCAACCAAGATTCACAGAGACAG 4257
Qy 4243 TGAAGCTGAGATGTAATGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGAG 4302
Db 4258 TGAAGCTGGAATGTAATGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGAG 4317
Qy 4303 TGCAGTATACATCTAATCAATGCAAAATCTGCAACGTTGATTTTCACTGTGACAAACAATG 4362
Db 4318 TGCAGTATACATCTAATGCAAAATCTGCAACGTTGATTTTCACTGTGACAAACAATG 4377
Qy 4363 GACTTATATAGAGCTGCGCCCATTTGGACACCCGTTACCTCACCCCTGTAATTTGT 4422
Db 4378 GACTTATATAGAGCTGCGCCCATTTGGACACCCGTTACCTCACCCCTGTAATTTAC 4437
Qy 4423 GTTATTAATCAATTAACCGGTTAATTCGTGCAATTGAACTTTGGTCTCATGTCTTATTA 4482
Db 4438 GTTATTAATCAATTAACCGGTTAATTCGTGCAATTGAACTTTGGTCTCATGTCTTATTA 4497
Qy 4483 TCTTATCTGCTCAACATAGCAACCGGTTAATCAATTAATGCTTGTGGCTGGCGCA - 4510
Db 4498 TCTTATCTGCTCAACATAGCTTAACATTAATGCTTGTGGCTGGCGCTA 4556
Qy 4541 -----ATACCCCTAGTATGAGTTGCCACTCCCTCTATGGCGGC 4581
Db 4557 AAAAGCTTAACATCGGCTTAACCCCTCTAGTATGAGTTGCCACTCCCTCTCTGGCGGC 4616
Qy 4582 TCGCTCGCTCGGTGGGCGCGGCAAGACAGAGCTCTGCGGTCTGCGGACTTTTGGTCCGA 4641
Db 4617 TCGCTCGCTCGGTGGGCGCGGCAAGAGTCCGAGAGCGGAGAGCTCTGCTCTGCC 4676
Qy 4642 GGGCCCAACGAGCGAGCGGCGGATGAGAGGATGGCCAA 4683
Db 4677 GGGCCCAACGAGCGAGCGGCGGATGAGAGGAGTGGGCAA 4718

RESULT 3
US-10-038-972A-12
; Sequence 12, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:

APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 4679
; TYPE: DNA
; ORGANISM: adeno-associated virus 2
US-10-038-972A-12

Query Match 70.4%; Score 3296.2; DB 3; Length 4679;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 3868; Conservative 0; Mismatches 803; Indels 20; Gaps 7;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCCGGGCGACCAAGTCCGCC 60
Db 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCCGGGCGACCAAGTCCGCC 60
Qy 61 CGAGCGCCGCGCTTTGCTCCGCGGCTCACTAGAGCGAGCGCGAGAGGAGTG 120
Db 61 CGAGCGCCGCGCTTTGCTCCGCGGCTCACTAGAGCGAGCGCGAGAGGAGTG 120
Qy 121 GCCAATCCCACTACAGGGGTTCTGAGGGGGTGGAGTGGTGAAGTAAATTCATAG 180
Db 121 GCCAATCCCACTACAGGGGTTCTGAGGGGGTGGAGTGGTGAAGTAAATTCATAG 180
Qy 181 GATTAGGAGAGTCTGTATTAGAGTCACTGAGTGTATTGCAATTTTGCAACAT 240
Db 181 GATTAGGAGAGTCTGTATTAGAGTCACTGAGTGTATTGCAATTTTGCAACAT 240
Qy 241 GTGTCAAGCTGGGTATTAAAGCCCGAGTGAACGACGAGGTTCCATTTTGAAGGGGA 300
Db 241 GTGTCAAGCTGGGTATTAAAGCCCGAGTGAACGACGAGGTTCCATTTTGAAGGGGA 300
Qy 301 GGTTTGAACGCGAG - GGCATGCGGGGGTTTACGAGATTGTATTAAGTCCCGACG 359
Db 301 GGTTTGAACGCGAGCGCGCATGCGGGGTTTACGAGATTGTATTAAGTCCCGACG 360
Qy 360 ACCTTGACGACATCTGCGCGCATTTCTGACAGCTTTTGAACCTGGGTGGCGAGAGG 419
Db 361 ACCTTGACGACATCTGCGCGCATTTCTGACAGCTTTTGAACCTGGGTGGCGAGAGG 420
Qy 420 AATGGAGTTGCGCGCATTTCTGACATGATCTGAATCTGAATCTGAATCTGAATCTGA 479
Db 421 AATGGAGTTGCGCGCATTTCTGACATGATCTGAATCTGAATCTGAATCTGAATCTGA 480
Qy 480 CCGTGGCGAGAGCTGACGCGGACCTTCTGAGTCCAGTGGCGCGGCGGAGTAAAGGCC 539
Db 481 CCGTGGCGAGAGCTGACGCGGACCTTCTGAGTCCAGTGGCGCGGCGGAGTAAAGGCC 540
Qy 540 CGAGAGCCCTCTTCTTGTTCAGTTTCAGTTTCAGTTCAGTTCAGTTCAGTTCAGTTC 599
Db 541 CGAGAGCCCTTCTTGTTCAGTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 600
Qy 600 TGTGAGACCAACGGGGTCAATTCATGCTGCTGGCGCTTCTGAGTCAATTAAGCG 659
Db 601 TGTGAGAAACACCGGGGTAAATTCATGCTTGTGGGACCTTCTGAGTCAATTAAGCG 660
Qy 660 ACAAGCTGGTGCAGACATCTACCGGGGATTCAGACCGGACCTTGCCAACTGGTTCGCG 719
Db 661 AAAAATGATTCAGAGATTTTACCGGGGATTCAGACCGGACCTTGCCAACTGGTTCGCG 720
Qy 720 TGAACCAAGACGCTAATGCGCGGAGAGGAGGAAACAAGTGTGAGAGAGTCTACATCC 779
Db 721 TCAAAAGACCAAGAAATGCGCGGAGGCGGAGAAACAAGTGTGAGAGTCTACATCC 780
Qy 780 CCAACTCTCTGCGCCCAAGACTCAGCGGAGCTGAGTGGGGTGAATTAACATGAGG 839

Db 781 CCAATTACTTGTCCCAAAACCAGCTGAGCTCCAGTGGCGTGAATAATGGAAC 840
QY 840 AGTATATAAGGCGGTTTAAACCTGCGCGAGCGCAAAAGCGCTCGGGCGCAGACTGA 899
Db 841 AGTATTAAAGCGCTGTGTTGAATCTCACGAGCGTAAAGGTGTGGGCGAGACTGA 900
QY 900 CCCAGTCAGCCAGACCCAGAGCAGAAACAGAGATCTGAATCCCAATTCAGACGCG 959
Db 901 CGCAGGTGCGAGACGAGAGCAGAAACAGAGATCAAGATCCCAATTCAGATGCC 960
QY 960 CTGTCACTCCGTCAAAAACCTCCGCACTGACATGAGCTGTGCGGTGGCTGTGAGC 1019
Db 961 CGGTCACTGATCAAAAACCTTCAAGCCAGTACATGAGCTGTGCGGTGGCTGTGAGC 1020
QY 1020 GGGGATCATCTCCAGAGAGCTGATTCAGAGAGAACAGGCTCTGTATCTCTTCA 1079
Db 1021 AGGGATTAACCTCGAGAAAGAGTGAATCAGAGAGAACAGGCTCTGTATCTCTTCA 1080
QY 1080 AGCGCGCTCCAACTCGCGGTCCAGATCAAGCGCTCTGGAACAATGCGCGAAGATCA 1139
Db 1081 ATGCGGCTCCAACTCGCGGTCCCAATCAAGGCTGTCTGTGAACAATGCGGAAAGATTA 1140
QY 1140 TGGCGCTGACCAAACTCGCGGTCCAGATCAAGGCTGTGAGCCGCTCGCGCGCAATTA 1199
Db 1141 TGAGCTGACCTAAACCGGCGGCTGACTGTGAGGCGAGCAAGCCGCTGTGAGCAATTT 1200
QY 1200 AAACCAACCGCATTTACCGCATCTGAGCTGAAGGCTGACGCTCTGTGCTACGCGGCT 1259
Db 1201 CAGCAATCGATTTATTAATTTTGAATCTAAACGGGTACGATCCCAATTTGCGGCTT 1260
QY 1260 CCGTCTTTCTCGGCTGGGCGCGAAAGGTTCGAGAAACGCAACACATCTGGCTGTTG 1319
Db 1261 CCGTCTTTCTGGGATGGGCGCAGAAAAGTTGCGAGAGAGAACACATCTGGCTGTTG 1320
QY 1320 GCGCGGCAACACGCGGCAAGACCAATCGCGAAAGCAATCGCGCGGCTGCGCTTCT 1379
Db 1321 GCGCTGCAACTACGCGGAAAGCAACATCGCGAGGCAATGCCACACTGTGCTTCT 1380
QY 1380 ACGGTGTGTCATCTGACCAATGAGAACTTCTCTTCAACGATTTGCGTCCGACAGATGG 1439
Db 1391 ACGGTGTGTCATCTGACCAATGAGAACTTCTCTTCAACGATTTGCGTCCGACAGATGG 1440
QY 1440 TGATCTGTGGGAGGAGCAAGATGACGCGCAAGGTGCTGAGTCCGCGCAAGCTTCC 1499
Db 1441 TGATCTGTGGGAGGAGGAGGAGATGACGCGCAAGGTGCTGAGTCCGCGCAAGCTTCC 1500
QY 1500 TCGGCGGACAGAGGTGCGCGTGAACCAAAAGTGCAGTCTGCGCGCAAGTCCCA 1559
Db 1501 TCGGAGGAAGCAAGGTGCGCGTGAACCAAAAGTGCAGTCTGCGCGCAAGTCCCA 1560
QY 1560 CCGCGGTGATCTGACCTTCCACACCAACATGTGCGCGTGAATGACGGAACAGACCA 1619
Db 1561 CTCCGCTGATCTGACCTTCCACACCAACATGTGCGCGTGAATGACGGAACAGACCA 1620
QY 1620 CTTTGAAGACACAGAGCGTGTGAGAGACCGGATGTTCAAAATTTGAATCTCAACGCGCTG 1679
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QY 1680 TGGAGCATGACTTTGGCAAGGTGACAAAGCAGAGAGTCAAAAGTCTTCCGCTGGGCG 1739
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QY 1740 AGGATCAGTGACCGAGGTGCGGCTGAGTCTACGTAAGAAAGGTGAGGACCAACCA 1799
Db 1741 AGGATCAGTGAGGTGAGGTCAGTGAATCTTACGTAAGAAAGGTGAGGACCAAGAA 1800
QY 1800 GACCGCGCGCGATGCGGATTAAGCGAGCCAGCGGCGCTGCGCTCAGTCCGCG 1859
Db 1801 GACCGCGCGCGATGCGGATTAAGTGAAGCCCAAGCGGTGCGGAGTCAAGTGGCG 1860
QY 1860 ATTCATGACGTGAGCGGAGAGAGCTCGGTGAGCTTGGCGCAGATGCCAAACA 1919
Db 1861 AGCCATCAGCGTCAAGACGCGGA--AGCTTGCATCACTACGACAGATGCCAAACA 1917

QY 1920 AATGTTCTGTCAGCGGCGCATGCTTCAGATGCTGTTCCCTGCAAAACATGCCAGAGAA 1979
Db 1918 AATGTTCTGTCAGCGGCGCATGAAATCTGATGCTGTTCCCTGCAAAACATGCCAGAA 1977
QY 1980 TGAATCAGAAATTTCAACTTTGCTTCAGCAGCAGGAGCAGAGACTGTTCAAGATGTTCC 2039
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QY 2040 CCGGCTGTCAGAACTCAACCGGT--GTCAGAGAGAGAGCTATCGAAACTGTG 2096
Db 2038 C---CGTCAAGAACTCAACCGGTTCTGTCTGTCAGAAAGCGGATCAGAAACTGTGCT 2094
QY 2097 CCAATTCATCTGTGTGGGCGGCTCCGAGATTTGCTGCTCGGCGCGCATCTGTC 2156
Db 2095 ACATTCATCATATCAAGGAGAAAGGTCAG--CGTTGCACTGCTGCAATCTGTGCA 2151
QY 2157 ACGTGAATCTGAGATGACTGTGTTCTGAGCAATTAATGACTTTAAACAGATATGGCTGCC 2216
Db 2152 ATGTGATTTGAGATGACTGCACTTTGAAACAATTAATGATTTAAATCAAGATGGCTGCC 2211
QY 2217 GATGTTATCTTCCAGATTTGCTCGAGGACAACTCTGAGAGGCAATTCGCGAGTGTGG 2276
Db 2212 GATGTTATCTTCCAGATTTGCTCGAGGACAACTCTCTGAAAGAAATTAAGACAGTGTGG 2271
QY 2277 GACTTGAAACCTGAGCGCGGCAACCCAAAGCCAAACGCAAAAGCAGAGAGAGCGCGG 2336
Db 2272 AAGCTCAACCTGCGCCCAACCAACAAAGCCGAGCGGCAATTAAGAGAGAGAGCG 2331
QY 2337 GGTCTGAGTCTTCTGCTGCTAACAATCTCGGACCTTCAACGAGACTGCAACAAGGAGAG 2396
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QY 2397 CCGCTCAACGCGGAGATGACGCGGCTCTGAGACAGCAAGGCTTACGACAGAGCTC 2456
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QY 2457 AAAGCGGTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2516
Db 2452 GACAGCGGAGCAACCGGTAACCTCAAGACCAACCGCGGAGTCTTCAAGAGGCG 2511
QY 2517 CTGCAAGAGATTAAGTCTTTTGGGAGCAACCTCGGAGAGAGCTTCTCAGGCGCAAGAG 2576
Db 2512 CTTAAAGAGATTAAGTCTTTTGGGAGCAACCTCGGAGAGAGCTTCTCAGGCGCAAGAG 2571
QY 2577 AGGTTCTCGAACCTTTTGTGCTGTGAGAGAGGTGCTAAGAGGCTCTGAGAAAGAA 2636
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QY 2637 GGTCCGTAAGAGAGTGGCGCACAGAGACCACTCTCTGCGGCAATTTGAGAGAGAGG 2696
Db 2632 AGGCGGTGAGAGACTCTCTGTGAGAGCAACCTCTCTGCGGCAATTTGAGAGAGAGG 2691
QY 2697 CAGAGCGCGCTAATAAAGAGACTCAATTTTGTGAGAGTCTGAGAGTCAAGTCAAGTCCC 2756
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QY 2757 GACCTCAACCTCTCGAGAGAACTTCAAGCAACCCCGCTGCTGTGAGAGCTTCAAGATG 2816
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QY 2877 GCTTCAAGAAATTTGAG 2936
Db 2872 TCTTGGAGAAATTTGAG 2931
QY 2937 ACCGGAACATGAGGCTTGGCGCACTTAAACAACCACTTAAACAAGCAAAATCTCAAGTCT 2996
Db 2932 ACCGGAACATGAGGCTTGGCGCACTTAAACAACCACTTAAACAAGCAAAATCTCAAGC 2991

OY	2997	TCAAACGGGGGACAGAACGACACACTATCTGGCTACACACCCCTGGGGTATTTT	3056
Db	2992	TCAC--GAGGCTCGAACGACATCATCTTTGGCTACACACCCCTTGGGGGATTTT	3048
OY	3057	GATTTCAACAAATTCACCTGCCATTTCTCACACGCTGACTGACGCACTCATCAACAC	3116
Db	3049	GACTTCACACAGTTTCACCTGCCATTTTACACAGTGACTGCAAAAGCTCATCAACAC	3108
OY	3117	AATTGGGGATTCGGGCCCAAGACCTCACTTCAAGCTCTTCACATCCAGTCAAGAG	3176
Db	3109	AACAGGGGATTCGACCCMAAGACTCAACTCAAGCTCTTTAACATTCAAGTAAAGAG	3168
OY	3177	GTCAAGAGAAATGATGGGCTGACGACCAATCGCTATAATCTTACAGACGGTTCAGTCC	3236
Db	3169	GTCAAGAGAAATGACGTAACGACGACATTCGCAATTACTTACAGACGGTTCAGTCC	3228
OY	3237	TTGTGGAAGCTGGAGTACCAAGTTCCCGTAAGTCTCGGCTCTGGGACACAGGCTGCTC	3296
Db	3229	TTTACTGACTCGGAGTACCAAGTCCCGTAAGTCTCGGCTCGGGGCAATCAAGATGCTCTC	3288
OY	3297	CCTCGGTTCCGGGCGGAGCGTGTTCATATTCGCGAGTACGGGCTACTAAGCTCAACAT	3356
Db	3289	CCGCGTTTCCAGACGAGAGTCTTATGAGTGCACAGTATGATATCTTACCTTGAACAC	3348
OY	3357	GGCAGCCAGGAGTGGAGCGCTCATCTTTTACTGCTGGAATAATTTCCATGCGAATG	3416
Db	3349	GGGAGTCAAGGAGTGGAGCGCTCTTCAATTTTACTGCTGAGATCTTTCTTTCAGATG	3408
OY	3417	CTGGAAGAGGGCAATACTTTTACCTTCAGCTACACCTTCGAGAGCGGCTTTCACACG	3476
Db	3409	CTGCGTACCGGAACAACTTTTACCTTCAGCTACATTTTGAAGAGTTCCTTTCACACG	3468
OY	3477	AGCTACGCGCACAGCCAGACGCTGGACCGGCTGATGAATCCCTCATGACCAATACCTG	3536
Db	3469	AGCTACGCTCACAGCCAGAGTGGAGCGGTCTCATGAATCCCTCATGACCAATACCTG	3528
OY	3537	TATTTCTGGAACAACTCTCAATATAGTCCGGAAGTCCCAAAACAGAACTTGCTGTTT	3596
Db	3529	TATTAATTGACAGCAACAACTCTCAAGTGAACCAACAGCAAGTCAAGCTTCAGTTT	3588
OY	3597	AGCGGTGGGTCTCCAGCTGGGATGTCGTTGAGCCCAAAAATGGCTACTGAGCCGCTG	3656
Db	3589	TCTCAGGCGGAGAGCAATGATCATTTGGGACCAAGTCTAGAACTGCTTCTGAGACCTGT	3648
OY	3657	TACCGGACGACGCGGTTTCTAAAACAAAAACAGCAACAACACGCAACTTATCTG	3716
Db	3649	TACCGCCACGACGCGATTCAAAAGCACTCTCGGATTAACAACAAGTAATCTCGTG	3708
OY	3717	ACTGGTGGTTAAAAATATACCTTATGGGGGTGAATATATATCAACCTCGGACGCT	3776
Db	3709	ACTGAGGCTAACATACCACTCTCATGAGCAAGACTCTCTGGTGAATCCGGGCCCGCC	3768
OY	3777	ATGGGCTCACAAAGACGACAAAGCAAGTCTTTTCCCATGAGCGGTGTCATGATTTT	3836
Db	3769	ATGGCAAGCCACAAAGACGATGAGAAAGTTTCTTCTCAGAGGGGTTCTCATCTTT	3828
OY	3837	GGAAAGAGACGCGCGAGCTTCAAACTGATTTGACATGTCATATATCAAGACGA	3896
Db	3829	GGGAAGCAGGCTCGAGAAAAAAATATGACATTTGAAAGTCAATATTTACAGACGA	3888
OY	3897	GAGGAATCAAAAGCACTTACCCGTGGCCACCGAAATTTTGGACTGTGGCACTCAAT	3956
Db	3889	GAGGAATCAAGAACCAATCCGTGGCTACGAGCAAGTATGTTTCTGTATCTTACCAAC	3948
OY	3957	CTCCAGAGCAGACACAGACCTCTGCGACCCGAGATGTCATGTTATGGAGCTTACT	4016
Db	3949	CTCCAGAGGCGAACAGACAGACGCTACCGCAATGTCACACACAGCGGTTCTTCCA	4008
OY	4017	GGAAATGATGGCAAGACAGAGAGTATACCTGCGAGGGTCCATTTTGGGCCAAATTCCT	4076
Db	4009	GGCAATGATTCGAGCAAGACAGATGTGATCTTACGGGGGCCCATCTGGGCCAAAGTTTCA	4068
OY	4077	CACACGATGACACTTTTACCCCGTCTCTCTCATGAGGCGGCTTTGACCTTACGCCG	4136

Db	4069	CACACGACGGACATTTTTCACCCCTCTCCCTCATTGGGTGATTTCGACCTTAAACACCC	4128
Qy	4137	CTCTCTCAGATCTCATCAAAAACACGCGCTGTTCTCTGGAATCCTCCGGCAGAGTTTTCG	4196
Db	4129	CCTCCACAGATTTCTCATCAAMAAACACCCGGGTACCTCGAATCCTTGACCACTTCA	4188
Qy	4197	GCTCAAAAGTTGGTCAATTATCATCACCCAGATTTCACAGACAAAGTAGGGTGAAT	4256
Db	4189	GGCGCAAGTTTGCTCTTCTCTCATACACAGTACTCCACGGGACAGGTCAAGGTGGAATC	4248
Qy	4257	GAATGGAGCTGCAGAAAGAAAACAGCAAAACGCTGGAATCCGATGTCAGTATACCT	4316
Db	4249	GAGTGGAGCTGCAGAAAGAAAACAGCAAAACGCTGGAATCCGAAATTCAGTACACTTC	4308
Qy	4317	AACATATGAAATCTGCCAACGTGATTTCACGTGTGACAAACATATGACTTTATATGAG	4376
Db	4309	AACATCAACAAGCTGTGTAATGTGACTTTACTGTGACACTAATGGCGGTATTCAGAG	4368
Qy	4377	CCTGCGCCCATATGGACACCCGTTTACCTCACCCGCTCGTAATGTGTGTTAATCAATA	4436
Db	4369	CCTGCGCCCATATGGACACCAAGTACTGACTGTAATCTGTATATGTTGTTAATCAATA	4428
Qy	4437	ACCGGTTAATTCGTGTCACTGGAACCTTGGTCTCATGTCTTATATCTTATCTGTGTAC	4496
Db	4429	ACCGTTTAAATTCGTTTCAAGTGAACCTTGGCTCTGTGGATTTCTTTCTTATCTAGTTTC	4488
Qy	4497	CATAGCAACCGGTATACATTAACCTGCTAGTGGCTGCGCTGCGCA----ATACCCCTAGT	4552
Db	4489	CATGGCTACGTAGATAGTATAGCAATGGCGGGTATATCATTTAATCAAGAACCTTGTGT	4548
Qy	4553	ATGAGATTGCCACTCCCTCTATACGCGGCTGCTGCTCGGTGGGCCGCGACAGCAGAG	4612
Db	4549	ATGAGATTGGCCACTCCCTCTCTGCGGGCTGCTGCTGCTCACTGAGGCGGGCGACCAAG	4608
Qy	4613	CTCTGCGGCTGCGGGAACCTTTGTCGCGAGGCCCCACCAAGCGAGCGAGCGCATAGAG	4672
Db	4609	GTCGCCGACGCCCGGGGCTTGGCCGGCGGCTCAAGTAGACGAGCGAGCGCAGAGAG	4668
Qy	4673	GGAGTGGCCAA 4683	
Db	4669	GGAGTGGCCAA 4679	
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; Sequence 2, Application US/09770315			
; Patent No. 6429001			
; GENERAL INFORMATION:			
; APPLICANT: Chiron Corporation			
; TITLE OF INVENTION: Recombinant AAV Packaging Systems			
; FILE REFERENCE: 20263-501			
; CURRENT APPLICATION NUMBER: US/09/770,315			
; CURRENT FILING DATE: 2001-01-26			
; PRIOR APPLICATION NUMBER: US 60/176,536			
; PRIOR FILING DATE: 2000-01-26			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 2			
; LENGTH: 8698			
; TYPE: DNA			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: recombinant DNA			
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Query Match 70.4%; Score 3296.2; DB 3; Length 8698;			
Best Local Similarity 82.5%; Pred. No. 0;			
Matches 3868; Conservative 0; Mismatches 803; Indels 20; Gaps 7;			
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Qy 3957 CTCAGAGCAGCAGACAGACCTGCGACCGGAGATGTGATGTATGGAGCTTAATCT 4016
Db 3949 CTCAGAGAGGCAACAAGAGAGCTACCGAGATGTCAACACAGAGCGTCTTCCA 4008
Qy 4017 GGAATGTTGGGCAAGCAGAGATTAATCTGCAAGGCTCTTAATTTGGGCAAAATTTCT 4076
Db 4009 GGAATGTTGGGCAAGCAGAGATTAATCTGCAAGGCTCTTAATTTGGGCAAAATTTCT 4068
Qy 4077 CACAGGATGAGACATTTCAACCCGCTCTCTCATGAGCGGCTTTGACTTAAGACCCG 4136
Db 4069 CACAGGATGAGACATTTCAACCCGCTCTCTCATGAGCGGCTTTGACTTAAGACCCG 4128
Qy 4137 CTTCTCAATCTCTCAATTAACAGCGCTGTTCTGCGAATCTCTCGGAGAGTTTGG 4196
Db 4129 CTTCTCAATCTCTCAATTAACAGCGCGCTGTTCTGCGAATCTCTCGGAGAGTTTGG 4188
Qy 4197 GCTCAAGTTTGTCTTCAATCAACCAATTTTCAACGAGCAAGGAGCGGAGAT 4256
Db 4189 GCTCAAGTTTGTCTTCTTCAATCAACCAATTTTCAACGAGCAAGGAGCGGAGAT 4248
Qy 4257 GAATGAGCTGCGAGAAAGAAACAGCAACGCTGATCCGAGTGCAGTATCT 4316
Db 4249 GAATGAGCTGCGAGAGAAAGAAACAGCAACGCTGATCCGAGTGCAGTATCT 4308
Qy 4317 AACTCAAAATCTGCAACGTTGATTTCACTGTGACAAACATGAGCTTTATCTGAG 4376
Db 4309 AACTCAAAATCTGTTATGTGACTTATCTGTGAGCACTAATGCGGTATCTGAG 4368
Qy 4377 CTTGCGGCAATTTGGCAACCGTTACTTCAACCGGCTCTGTAATTTGTTAATCAATA 4436
Db 4369 CTTGCGGCAATTTGGCAACCGATTTCTGATCTGTAATTTGTTAATCAATA 4428

OY	4437	ACCGTTAAATCGGTGCACTTGAGTGCATAATGCCATTATATCTTAATGTCAC	4438
Dd	4429	ACCGTTAAATCGTTCACTTGAGTGCATAATGCCATTATATCTTAATGTCAC	4488
OY	4497	CATAGCAAACGGATTACACATTACTGCTTAGTGGCTTCGGA---ATACCCTACTG	4552
Dd	4489	CATGGCTCAGTAGAATAATAGCATGGCGGTTAATCATTAACAAGAACCCCTAGT	4548
OY	4553	ATGAGATTGCCCATCCTCTTAATGGCGCTGCTGCTCGGTGGGCGCGGACAGACAG	4612
Dd	4549	ATGAGATTGCCCATCCTCTCTGCGCCTGCTGCTCACTAGAGCGCGGCGACCAAG	4608
OY	4613	CTCTGCCCTGCGGACCTTTGGTCCGAGGCCACCGAGCGAGCGACGACATAGAG	4672
Dd	4609	GTCGCCCGACCGCGGCTTTGCCGCGGCTCAGTAGAGAGCGAGCGCGACGAGAG	4668
OY	4673	CGAGTGGCCAA	4683
Dd	4669	GGAGTGGCCAA	4679

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RESULT 5-
US-09-717-789C-25
; Sequence 25, Application US/09717789C
; Patent No. 6984517
; GENERAL INFORMATION:
; APPLICANT: Chorini, John
; APPLICANT: Kotlin, Robert M.
; APPLICANT: Saefer, Brian
; TITLE OF INVENTION: AAYS VECTOR AND USRS THEREOF
; FILE REFERENCE: 14014.032U3
; CURRENT APPLICATION NUMBER: US/09/717,789C
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 4679
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6984517e =
; OTHER INFORMATION: synthetic construct
; US-09-717-789C-25

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Query Match	70.38	Score 3293	DB 4	Length 4679
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Matches 3866; Conservative 0; Mismatches 805; Indels 20; Gaps 7;

Qy	TTGGCAGCTCCCTCTGTGGAGCTGCGTCGCTCACTAGAGGCGGGCGACAAAGATGCGC	60
Db	1 TTGGCAGCTCCCTCTGTGGAGCTGCTGCTCACTAGAGGCGGGCGACAAAGATGCGC	60
Qy	CGACGCCCGGGCTTTTGCCTCCGGGCGGCTTCAGTGAACGAGCGCGACGAGAGGAGTG	120
Db	61 CGACGCCCGGGCTTTTGCCTCCGGGCGGCTTCAGTGAACGAGCGCGACGAGAGGAGTG	120
Qy	CGACGCCCGGGCTTTTGCCTCCGGGCGGCTTCAGTGAACGAGCGCGACGAGAGGAGTG	120
Db	61 CGACGCCCGGGCTTTTGCCTCCGGGCGGCTTCAGTGAACGAGCGCGACGAGAGGAGTG	120
Qy	121 GCCAATCTCCATCATCTAGGGGTTCTCTGAGAGGGTGGAGTCTGAGCTGAATTAGCTCATAG	180
Db	121 GCCAATCTCCATCATCTAGGGGTTCTCTGAGAGGGTGGAGTCTGAGCTGAATTAGCTCATAG	180
Qy	121 GCCAATCTCCATCATCTAGGGGTTCTCTGAGAGGGTGGAGTCTGAGCTGAATTAGCTCATAG	180
Db	121 GCCAATCTCCATCATCTAGGGGTTCTCTGAGAGGGTGGAGTCTGAGCTGAATTAGCTCATAG	180
Qy	181 GGTATTAGGAGAGTCTGTATTAGAGGTCAAGTGAAGTTTTCGACATTTTTCGACACCAT	240
Db	181 GGTATTAGGAGAGTCTGTATTAGAGGTCAAGTGAAGTTTTCGACATTTTTCGACACCAT	240
Qy	181 GGTATTAGGAGAGTCTGTATTAGAGGTCAAGTGAAGTTTTCGACATTTTTCGACACCAT	240
Db	181 GGTATTAGGAGAGTCTGTATTAGAGGTCAAGTGAAGTTTTCGACATTTTTCGACACCAT	240
Qy	241 GTGGTCAACGCTGGGATTTTAAAGCCGAGTGAGCAGCAGAGGCTTCCATTTTTGAAGCCGGA	3000
Db	241 GTGGTCAACGCTGGGATTTTAAAGCCGAGTGAGCAGCAGAGGCTTCCATTTTTGAAGCCGGA	3000
Qy	241 GTGGTCAACGCTGGGATTTTAAAGCCGAGTGAGCAGCAGAGGCTTCCATTTTTGAAGCCGGA	3000
Db	241 GTGGTCAACGCTGGGATTTTAAAGCCGAGTGAGCAGCAGAGGCTTCCATTTTTGAAGCCGGA	3000

QY	301	GGTTGAACGGCGAG - GGCATGCGGGGGTTTACGAAATTGTGATTTAAAGTCCACAG	359
Db	301	GGTTTGAACGGCACCGCCCATGCGGGGGTTTACGAAATTGTGATTTAAAGTCCACAG	360
QY	360	ACCTTGAAGACATCTGCGCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAAG	419
Db	361	ACCTTGAAGGGGATCTGCGCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAAG	420
QY	420	AATGGAGATTGCGCCAGATTCTGCATATGATCTTGAAATCTGATTGAGCAGGCACTCTGA	479
Db	421	AATGGAGATTGCGCCAGATTCTGCATATGATCTTGAAATCTGATTGAGCAGGCACTCTGA	480
QY	480	CCGTGGCCGGAAGAGTGTGAGGCGCATCTTCGTGTCACTGGCGCCGCGTGAAGTAAAGGCC	539
Db	481	CCGTGGCCGGAAGAGTGTGAGGCGCATCTTCGTGTCACTGGCGCCGCGTGAAGTAAAGGCC	540
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Db	541	CGSAGGCCCTTCTTCTTTGTTCAGTTTCGAGAAGGGCGAGTCTTCCATATGCACTGCTCC	600
QY	600	TGTTGAGAACCA CGGGGGTCAAAATCCATGTGTCTGGGC CGCTTCTTGAGTCAGATTGACG	659
Db	601	TCGTGAAACCACCGGGGTGAATTCATGGTTTGGGACGTTTCTCGATGCAGATTCCGC	660
QY	660	ACAAGCTGTGTCAACCATCTACCGCGGGATTCGAGCCGACCTTGCCCACTGTGTTCGGG	719
Db	661	AAAACTGATTTCAAGGAATTTTACCGCGGGATTCGAGCCCATCTTTGCGAAACTGTGTTCGGG	720
QY	720	TGACCAAGACGGTAAATGGCGCGCGAGGGGGGAAACAAGGTGTGTGAAGAGTCTACATCC	779
Db	721	TCACAAAGACCAAGAAATGCGCCGGAGCGGGAACAAAGTGTGTGAATGATGTCTACATCC	780
QY	780	CCAACTACCTCTGCGCCCAAGACTGACGCCGAGCTGCAGTGGCGGTGACTTAACTAGAGAG	839
Db	781	CCAATTACTTGTCTCCCAAAACCCAGCTGAGCTCAGTGGCGGTGACTTAAATGAGAAC	840
QY	840	AGTATATTAAGCGCGTGTTTAAACTGTGGCCGACCGCAACCGCTGTGTGGCGACGACTGA	899
Db	841	AGTATTTTAAAGCGCGTGTTTGAATCTCAGCGAGCGCTTAAACGGTGTGTGGCGGACGACTCTGA	900
QY	900	CCCAAGTACAGCAACCCAGGAGAGAACAGAGGAATCTGAACCCCAATTCTGACGGGC	959
Db	901	CGACAGTGTGCAACCGAGGAGCAAAACAAAGAAATCAAAATCTCAATTTCTGATGGGC	960
QY	960	CTGTATCTCCGTCAAAAAATCTCCGACGCTCATATGAGCTGTGGGTGGCTGTGTGACC	1015
Db	961	CGGTGATCAAGTCAAAAATCTTACGCGAGTACATATGAGCTGTGGGTGGCTGTGTGACA	1022
QY	1020	GGGGCATCACTCCGAGAGAGATGATTCAGAGAGACCAAGGCTCTGTATCTTCTTCA	1075
Db	1021	AGGGGATTAATCTCGAGAGAGATGATTCAGAGAGACCAAGGCTCTATATCTTCTTCA	1080
QY	1080	ACGCGGCTCTCCAATCTCGCGGTCCAGATTCAGAGCGGCTGTGTGACAAATGCCGGAAGATCA	1133
Db	1081	ATGCGGCTCTCCAATCTCGCGGTCCCAAAATCAAGGCTGCTTGTGACAAATGCCGGAAGATTA	1140
QY	1140	TGGCGCTGACCAAAATCGCGCGCGACATCACTGTAGGCGCGGCTCCGCGCGCGCATTA	1199
Db	1141	TGAGCTGTACTTAAACCGCCCCGACTCTGTGTGGGCGACAGCGCTGTGAGACATTT	1200
QY	1200	AAACCAACCGCATTTACCGCATCTCTGTGAGCTGAACCGGTACGACCTTGCTTACGCGGCT	1259
Db	1201	CCAGCAATTCGGAATTTATTAATTTTGTGAACTTAAACGAGTACGATCCCAATATGCGGGCT	1260
QY	1260	CCGTCTTTTCTGTGCTGGGCGCAAAAAGGTTCCGAAAAACGCAACCATCTGTGCTGTTTG	1319
Db	1261	CCGTCTTTTCTGTGAGTGGGCGACGAAAAAGTTTCGCAACAGGAAACCACTGTGCTGTTTG	1320
QY	1320	GGCGGCGCACACGGGGCAAGACCAACATCGCGGAAAGCATGCGGCACGCGGTGCGCTTCT	1379
Db	1321	GGCTGTGACCTACCGGGAAAGCAACATCGCGAGGCGCATATGCCCAACTGTGTGCTTCT	1380
QY	1380	ACGGCTCGTCAACTGAGCCAATGAGACTTTCCCTTCAACGATTTGCTGTGACAAGATGG	1439

Db 1381 ACGGCTGCTAACTGAGCAATGAGAACTTTCCCTTCAACGACTGTCTCCAGCAAGATGG 1440
Qy 1440 TGAATTCGTGGAGAGAGGCAAGATGACGCGCCAGAGTGTGAGATTCGCCCAAGGCATTC 1499
Db 1441 TGAATTCGTGGAGAGAGGCAAGATGACGCGCCAGAGTGTGAGATTCGCCCAAGGCATTC 1500
Qy 1500 TCGGCGAGAGCAAGGTGGCGCTGAGCAAAAAGTCAGATCGTCCGCCAGATTCGATCCA 1559
Db 1501 TCGAGAGAAAGCAAGTGGCGCTGAGCAAAAAGTCAGATCGTCCGCCAGATTCGATCCA 1560
Qy 1560 CCCCCGTGATGTCCTTCACCAACCAATGTGCGCGTGAATTCGAGGAAACAGACCA 1619
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Db 1621 CTTTGGAGACACAGAGCGGTGGAGAGCCGGAATGTTCAAAATTTGAATTCACCCGCTC 1680
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Db 1681 TGAATCAGATCTTTGGAAAGTCAACCAAGCAGAAAGTCTTCCGCTGGCGC 1740
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Db 1741 AGGATCAGTGTGAGGTGGAGCATGATTCATCTCAAGAAAGGTGAGCCAAAGAAA 1800
Qy 1800 GACCCGCCCCGATGAGCGGATTAAGCGAGCCCAAGCCGCTGAGCGCGG 1859
Db 1801 GACCCGCCCCGATGAGCGGATTAAGCGAGCCCAAGCCGCTGAGCGCGG 1860
Qy 1860 ATCCATTCAGCTCAGACCGAGAGAGCTCCGCTGAGCTTTCGCCAGAGTACCAAAACA 1919
Db 1861 AGCCATTCAGCTCAGACCGAGAGAGCTCCGCTGAGCTTTCGCCAGAGTACCAAAACA 1917
Qy 1920 AATGTTCTGTCACGCGGCGATGCTTCAGATGCTGTTTCCGCAAAACATGCGAGAGAA 1979
Db 1918 AATGTTCTGTCACGCGGCGATGATGATGCTGTTTCCGTCAGACAAATGCGAGAGAA 1977
Qy 1980 TGAATCAGAAATTTCAACTTTGCTTCAGCAGCGGAGCAGAGACGTTCAAGATGTTTCC 2039
Db 1978 TGAATCAGAAATTTCAAAATCTGCTTCACCTCAGCAGAGAAAGCTGTTAAGATGCTTTC 2037
Qy 2040 CCGGCTGTGAGAAATCTCAACCGGT---CGTCAGAAAGAGAGCTGATGAGAACTGTG 2096
Db 2038 C---CGTGTCAAGAAATCTCAACCGGTTCGTCTGTCAAAAAGCGATTCAGAAATCTGTCT 2094
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Qy 2157 ACGTGAATCTGGAATGACTGTGTTCTGAGCAATTAAGTCTTAAACAGAGTATGGCTGCC 2216
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Db 2452 GACACGAGAGCAACCCGTACTCTAAGTACAAACACCGCAGCGAGTTTCAGAGCGC 2511
Qy 2517 CTGCAAGAAATACGTCTTTTGGGGGCAACCTGGGGGAGCAGCTTTCAGGCGAAGAG 2576
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Qy 2577 AGGTTCTCAACCTTTTGGTCTGTGTGAGAAAGTCTTAAGACGCTCTCTGAGAAAGAA 2636
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Qy 2637 GTCCTGTAAGACGTGCGCAAGAGACGAGCTCTCTCTGGGCAATTCGCAAGACAGC 2696
Db 2632 AGGCGGTGAAGCACTCTCTGTGTGAGACGAGCTCTCTCTCGGGAACCGGAAAGCGGCG 2691
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Db 2692 CAGCAGCTTGCAGAAAGAAATGAAATTTGTGAGCTGAGCTGAGAGCGAGCTAGTACT 2751
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OY 3597 AGCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAAGTGGTACCTGGACCCGT 3656
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OY 3777 ATGGCTCAACAACAAAGACAAAGCAAGTCTTTCCATAGGGGGTGTGATTTT 3836
DB 3769 ATGGACAGCCACAAAGACATAGAAAGATTTTCTCAAGAGGGGGTCTCACTTT 3828
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DB 4489 CATAGCTATGATATGATAGATGCGGGGTTAATCAATTAATCAAGAACCCCTAGTG 4548
OY 4553 ATGAGATTGCCACTCCCTATATGCGGCTGCTGCTGCTGAGGCGCGGACAGACAG 4612
DB 4549 ATGAGATTGCCACTCCCTATATGCGGCTGCTGCTGCTGAGGCGCGGACAGACAG 4608
OY 4613 CTTCGCGTCTGCGGACCTTTGTGTGCGAGGCGCGACAGAGACGAGCGCGCAATAG 4672
DB 4609 GTTCGCGGACCGCGGCGTTTTCGCGGCGGCTTCAATGAGGAGCGAGCGCGAGAG 4668
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OY 4673 GGAGTGCCAA 4683
DB 4669 GGAGTGCCAA 4679

RESULT 6
US-08-254-358-1
; Sequence 1, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,358
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658785and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-254-358-1

Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;
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OY 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAAGAGTCCG 60
DB 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAAGAGTCCG 60
OY 61 CGAGCGCGGCGCTTTCGCGGCGCGCTCACTGAGCGAGCGCGGAGAGGAGT 120
DB 61 CGAGCGCGGCGCTTTCGCGGCGCGCTCACTGAGCGAGCGCGGAGAGGAGT 120
OY 121 GCCAATCATCACTAGAGGCTTCTGAGAGGCTGAGTCTGAGTGAATTAAGTCAATAG 180
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OY 121 GCGAAGCGGCTTTCGCGGCGCGCTCACTGAGCGAGCGCGGAGAGGAGT 120
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OY 181 GGTAGGAGAGTCTGTATTAAGAGTCACTGAGTGTTCGACATTTTCGACACCAT 240
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OY 241 GTGATCAGCGGGATTTTAAGCCGAGTGAAGCAAGGCTCCATTTTGAAGCGGGA 300
DB 241 GTGATCAGCGGGATTTTAAGCCGAGTGAAGCAAGGCTCTCCATTTTGAAGCGGGA 300
OY 301 GGTTTGAACGCGCAG-CGCCATGCGGGGTTTTCAGAGATTGATTAAGGTCCCAAGCG 359
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Db 301 GATTGAAAGCGAGCCGCCATGCGGGGTTTACGATGTGTGATTAAGTCCCAAGCG 360
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Db 361 AACTTGAGAGCATGCGCCGATTTCTGACAGCTTTGTGAACCTGGGGTGGCCGAGAGG 420
Oy 420 AATGGAGTTGGCCGACAGATTTCTGACATGATCTGTAATCTGATTTGAGAGGACCCCTGA 479
Db 421 AATGGAGTTGGCCGACAGATTTCTGACATGATCTGTAATCTGATTTGAGAGGACCCCTGA 480
Oy 480 CCGTGGCCGAGAGCTGACAGCGGCACTTCTGCTGTCACATGCGCGCCGCTGATGAAGGCC 539
Db 481 CCGTGGCCGAGAGCTGACAGCGGCACTTCTGACGGAATGGCGCCGTGTGATGAAGGCC 540
Oy 540 CGGAGGCGCTCTTCTTGTGATGTTGAGAGGGGAGATCTCACTTCCACTCCATATTC 599
Db 541 CGGAGGCGCTCTTCTTGTGATGTTGAGAGGGGAGAGTCACTTCCACTGACGTC 600
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Oy 960 CTGTATCATCGGTCAAAAACCTCCGACGCTACATGAGACTGATGGATGGCTGTGAGAC 1019
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Db 2452 GACAGCGGAGAGCAACCGGATCTCAAGTACACAGCGCGAGGAGTTTCAGAGAGCGC 2511

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OY	2517	AGGGTCTCGAACCTTTTGGTCTGGTTAGGAAAGGTGCTAAAGAGGGCTCTGGAAAGAA	26366
Db	2512	AGGGTCTTGAACCTCTGGGCTGGTTAGGAACTGTTAAGACGGCTCCGGGAAAAAG	26311
OY	2637	CGTCCGGTAGAGCACTGCCACAAAGCCAGACCTCTCCTCGGGCATTTGGCAAGCAGGC	26366
Db	2632	AGCGCGTAGAGCACTCTCTGTGTGAGCGACACTCTCCTGGGAAACCGGAAAGCGGGC	26911
OY	2637	CAGCAGCCCCGCTAAAAAGAGACTCAATTTGGTCAACTGGGCACTCAGAGTCAGTCCC	27566
Db	2632	CAGCAGCCTCGAAGAAAAAGATTGAATTTGGTCACTGGAGAGCGCAGACTCAGTACCT	27511
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Db	2812	GCTACAGGCAATGGGGGACCAATGGCACAATAAGAGGGCGCCGAGAGGTGGGTAT	28711
OY	2817	GCTTCAGGAAATTGGCATTTGGCATTCACATGGCTGGGCGACAGATCATCACACAGC	29366
Db	2812	TCCTTCGGAAATTGGCATTTGGCATTCACATGGATGGGCGACAGAGTCATCACACAGC	29311
OY	2937	AACCGAATATGGGCGCTTGGCCCACTATTAACAACAACCTCTACAGCAATCTCCAGTCT	29966
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OY	3057	GATTTCACACAGATTCACCTGCCATTTCTCACACGTGATGGCAGACGATCATCAACAC	31166
Db	3049	GACTTCACACAGATTCACCTGCCATTTTCAACAAGTATGGCAAAAGCTCATCAACAC	31086
OY	3117	AATTGGGATTTCCGGCCCCAAGAGACTCACTTCAAGCTTTCAACATCAAGTCAAGAG	31766
Db	3109	AACGGGGATTTCCGACCCMAAGACTCACTTCAAGCTTTTAACTTCAAGTCAAAAGAG	31686
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OY	3237	TTGTTCGACTCGAGTACCAAGTTCCTCCGATGCTCTCGGCTCTGGCGCACAGAGGCTGC	32966
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OY	3237	CCTCCGTTCCGGGGGAGCGTGTTCATGATTCGACAGTACGGCTACTAAGCTCAACAT	33566
Db	3289	CCGCGTTTCCAGACGAGCGTCTTATGATGGCGACAGTATGATCTCTCAACCTCAAAAC	33486
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OY	3477	AGCTACCGGCGACAGCGAGAGCTTGGACCGGCTGATGAATCTCTCATGACAGATCCTG	35366
Db	3469	AGCTACGCTCAAGCGAGAGTCTGGACCGGTCTCATGATCTCTCATGACAGATCCTG	35286
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Db	3949	CTCCAGAGGCAACAGACAAGACTCCAGATGTCAACACACACAGAGGCTTCTTCCA	4008
Oy	4017	GGAAATGTGTGGCAAGACAGAGATTAATCCAGGGGTCTATTTGGGCCAAATTCCT	4076
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Oy	4077	CACACGATGAGCACTTTCAACCCGCTCTCTCTCAATGGCGGCTTGTGACTTAAGACCCG	4136
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Oy	4137	CCTCTCAGATCTCATTAATAAACAAGCTGTTCCTGTGGAATCCTCGGCAAGTTTTCG	4196
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Db	4369	GCTTCGCCCATTTGGCAACCAATCTGACCTGTAAATCTGTAAATGCTTGTAAATCATA	4428
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Oy	4552	GATGAGTTCGCCACTCCCTTATGCGCGCTCTCGTCTCGTGGTGGGCGCGGACAGCAGA	4611
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RESULT 7
US-08-475-391-1
; Sequence 1, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578621land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-475-391-1
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Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;

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Db 2392 CCGGTCAACGAGAGAGAGAGCGCGCGGCTCGAGACGACAAAGGCTTACGACAGAGCTC 2451
Qy 2457 AAAGCGGTGACATCCGTACTGCGGTATTAACAGCGCGACGCGGAGTTTCAGAGCGT 2516
Db 2452 GACAGCGGAGAGAACCCGTACTCAAGTAAACAGCGCGAGCGGAGTTTCAGAGCGC 2511

Qy 2517 CTGCAAGAGATGAGTCTTTTGGGGGCAACCTCGGGGAGAGAGTCTTCAGGCCAAGAG 2576
Db 2512 CTTAAAGAGATGAGTCTTTTGGGGGCAACCTCGGAGAGAGAGTCTTCAGGCCAAGAG 2571
Qy 2577 AGGGTCTCGAACCCTTTTGTCTGGTTGAGAGAGGTGCTTAAGACGGCTCTTGAAAGAA 2636
Db 2572 AGGGTCTTGAACCTCTGGGCTGGTTGAGAGACCTGTTAAGACGGCTCCGGGAAAAAG 2631
Qy 2637 GGTCCGTTAAGAGCACTGCCCAAGAGCGAGACTCTCTCTGGGGATGAGCAAGAGC 2696
Db 2632 AGGCGGTAGAGCACTCTCTGTGAGCGAGACTCTCTCTCGGGAACCGGAAAGCGGCG 2691
Qy 2697 CAGAGCCCGCTAAAGAGACTCAATTTTGTGAGAGTGGGAGCTGAGAGTCTGCC 2756
Db 2692 CAGAGCCCGCTGAGAGAGATTTGATTTTGTGAGAGTGGGAGCTGAGAGTCTGCC 2751
Qy 2757 GACCCACAACTCTCGAGAACTTCAGCAACCCCGCTGCTGAGGACTTAACAATG 2816
Db 2752 GACCCCGAGCTCTCGAGCAAGCAACAGCAACCCCGCTGCTGAGGACTTAACAATG 2811
Qy 2817 GCTTCAAGCGGTGGCGCACTATGCGAGACATTAACGAGCGCGAGAGTGGTAT 2876
Db 2812 GCTTCAAGCGGTGGCGCACTATGCGAGACATTAACGAGCGCGAGAGTGGTAT 2871
Qy 2877 GCTTCAAGAAATTTGAGATTTGAGATTTCCATGCGCGGCGAGAGTCAACCAAGC 2936
Db 2872 TCTTCGGAATTTGAGATTTGAGATTTCCATGAGTGGCGAGAGTCAACCAAGC 2931
Qy 2937 ACCGAGCATGGGCTTGCCCACTTAACAACCACTCTTAACAAGCAATCTCCAGTCT 2996
Db 2932 ACCGAGCATGGGCTTGCCCACTTAACAACCACTCTTAACAAGCAATCTCCAGTCT 2991
Qy 2997 TCAACGGGGGCGAGCAAGCAACCACTTAACAGTCTTCCAGTCTTCCAGTCTT 3056
Db 2992 TCA---GGAGCTGGAACGAGCAATCACTTGTGCTTACAGACCCCTTGGGGGATTTT 3048
Qy 3057 GATTTCAACAGATTCACGCTGATTTCTCAACAGTGCAGGAGCTGATCAACAGC 3116
Db 3049 GATTTCAACAGATTCACGCTGATTTCTCAACAGTGCAGGAGCTGATCAACAGC 3108
Qy 3117 AATTGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAATCCAGAG 3176
Db 3109 AATTGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAATCCAGAG 3168
Qy 3177 GTCAAGAGATGATGCGCTCAAGCAATGCTTAATACTTTACAGAGCGGTTCAAGT 3236
Db 3169 GTCAAGAGATGATGCGCTCAAGCAATGCTTAATACTTTACAGAGCGGTTCAAGT 3228
Qy 3237 TTTGCGAGCTGGAGTACCAAGTCCCGTCCGCTCGGCGACCAAGGCTGCTC 3296
Db 3229 TTTGCGAGCTGGAGTACCAAGTCCCGTCCGCTCGGCGACCAAGGCTGCTC 3288
Qy 3297 CCTCCGTTCCCGGGGAGAGTGTGATTAATCCGAGTACGAGTCAACCTCAACAT 3356
Db 3289 CCGCGTTCCAGAGAGAGTGTGATTAATCCGAGTACGAGTCAACCTCAACAT 3348
Qy 3357 GGCAGCAGAGAGTGGAGCGCTCATCTTTTATGCTGCAATATTTCCATGCGAGATG 3416
Db 3349 GGCAGTCAAGAGAGAGCGCTCTTCAATTTTATGCTGCAATATTTCCATGCGAGATG 3408
Qy 3417 CTGAGAACGGGCAATTAATCTTACCTTCAAGTCAACCTTCAAGAGAGGCTTCAAGC 3476
Db 3409 CTGAGTACGGGCAATTAATCTTACCTTCAAGTCAACCTTCAAGAGAGGCTTCAAGC 3468
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Db 3469 AGCTACGCGTCAACAGAGTGTGAACGCTCATGATGATCTCTCATACGACCAATACCTG 3528
Qy 3537 TATTAACCTGAACAGAACTCAATCAAGTCCGGAAGTCCCAAAACAGAGCTTCTGTTT 3596
Db 3529 TATTAACCTGAACAGAACTCAATCAAGTCCGGAAGTCCCAAGGCTTCAAGTCTT 3588

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QY 3597 AGCCGCTGCTCCAGCTGGAGTGTCTGTCAGCCCAAAAACCTGGCTACTGGAACCCCTGT 3656
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QY 3717 ACTGGTGTCAAAATATACTTAATGAGGGGTGAATCTTAATCAACCCCTGGCACTGCT 3776
Db 3709 ACTGAGCTTACCAAGTACCACTCTCAATGACAGAGACTCTGTGGTAATCCGGGCGCCGC 3768
QY 3777 ATGGCTTCAACAAGACGACAAAGCAAGTCTTCTTCCATGAGCGGTGTGATGATTTT 3836
Db 3769 ATGGCAAGCCCAACAAGGACGATGAAGAAAAGTTTTTCTCAGAGGGGTTCTCATCTTT 3828
QY 3837 GGAAGAGAGAGCGCGGAGCTTCAAACTGCTGACAAATGTCATATACACAGACGA 3886
Db 3829 GGGAGGCAAGGCTCAGAGAAAACAAAATGTGAACATTTGAAAAGTTCATATTAACAGACGA 3888
QY 3897 GAGGAATCAAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCACTCAAT 3956
Db 3889 GAGGAATCGAACAACCAATCTCGGTGCTAGGAGCACTATGTTCTGTATCTAACAC 3948
QY 3957 CTCCAGAGCAGCAGACAGACCCCTGCGACCGGAGATGTGACATGTTATGGAGCCCTTACT 4016
Db 3949 CTCCAGAGAGGCAACAGACAGCTACCGGAGATGTCAACAACAAGGGTCTTCTCA 4008
QY 4017 GGAATGTGTGTGGCAAGACAGACGTAATCTGACGGGTCTTATTTGGGCCAAATTTCT 4076
Db 4009 GGCATGTGTGTGGCAAGACAGATGTGACCTTTCAGGGGCCCATCTGGGCAAAAGTTCCA 4068
QY 4077 CACACGATGAGCACTTTCACCCCGTCTCTCTCAATGGCGGCTTTGACTTAAGACCCG 4136
Db 4069 CACACGAGCAGACATTTTCAACCCCTCTCTCTCATGCTGATTCGACTTAACACCTT 4128
QY 4137 CCTCTCAGATCTATCAAAAACAACGCTGTCTCTCGGAATCTCTCGGACAGATTTTCG 4196
Db 4129 CCTCCACAGATCTCATCAAGAAACACCCCGGACTCTGGAAATCTTGCACACCTTCACT 4188
QY 4197 GCTACAAAGTTGCTTCTTATCATCAACCAATTCACAGACA-AGTGAACGTGTGAGAT 4255
Db 4189 GCGGCAAAAGTTGCTTCTTATCATCAACAGTACCAAGGACACGCTCACGCTGGAAT 4248
QY 4256 TGAATGGAGGCTGCGAAGAAAACAGCAAAACGCTGGAATCCCGAAGTGCAGTATAC 4315
Db 4249 CGAATGGAGGCTGCGAAGAAAACAGCAAAACGCTGGAATCCCGAATTCAGTACCTTC 4308
QY 4316 TAACTATGCAAAATCTGCCAAAGTTGATTTCACTGTGACAACAATGCACTTTTATCTGA 4375
Db 4309 CAACCTAACAAAGTCTGTTAATCGTGACTTACCGTGTGATCTAATGCGTGTATTGACA 4368
QY 4376 GCTCTGCCCCATTTGGCAACCCGTACTCAACCCGTCCCTGTAAATTTGTGTATTCATA 4435
Db 4369 GCTCTGCCCCATTTGGCAACCAATCTGATCTGTAAATGCTTGTAAATTCATA 4428
QY 4436 AACCGTTAATTCGTGCTAGTTGAACCTTGGTCTCATCTCTATATCTTATCTATCTGCA 4495
Db 4429 AACCGTTAATTCGTGCAAGTTGAACCTTGGTCTCTGCTATTTCTTCTTATCTAGTTT 4488
QY 4496 CCATAGCAACCGGTTACCATTAATCTGTTAGTGGCGCTTGCAG-ATACCCTTAACT 4551
Db 4489 CCATAGGCTAAGTAAATATTAAGCATGGCGGTTAATTAATTAATCAAGAAACCCCTAGT 4548
QY 4552 GATGAGTTGGCCCACTCTCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4611
Db 4549 GATGAGTTGGCCCACTCTCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4608
QY 4612 GCTCTGCGCTGCGGACCTTGTGCTGCGGACCCCAACGAGCGAGCGGCGCATGGA 4671
Db 4609 GGTGCGCGGACGCGCGGCTTGGCGGCGGCTTCACTGAGCGAGCGAGCGGCGGAGGA 4668
QY 4672 GGGAGTGGCCAA 4683
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Db 4669 GGGAGTGGCCAA 4680

RESULT 8
US-08-709-609-1
; Sequence 1, Application US/08709609
; Patent No. 5858775
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858775and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-709-609-1

Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;

QY 1 TTGGCCACTCCCTCTGCGCGCTGCTGCTCACTGAGCCGGGCGACCAAGTGGCC 60
Db 1 TTGGCCACTCCCTCTGCGCGCTGCTGCTCACTGAGCCGGGCGACCAAGTGGCC 60
QY 61 CGAGCGCCGGGCTTTGCCCGGGCGGCTCACTGAGCGAGCGGCGGCGAGAGGAGTG 120
Db 61 CGAGCGCCGGGCTTTGCCCGGGCGGCTCACTGAGCGAGCGGCGGCGAGAGGAGTG 120
QY 121 GCGCACTCCATCACTAGGGGTTCTGAGAGGGTGTGAGTCTGTGACGTAAATAGTCA 180
Db 121 GCGCACTCCATCACTAGGGGTTCTGAGAGGGTGTGAGTCTGTGACGTAAATAGTCA 180
QY 181 GGTAGGAGAGTCTGTATTAGAGGTACGTAGTGTGTTTGGCATTTTGGCACACAT 240
Db 181 GGTAGGAGAGTCTGTATTAGAGGTACGTAGTGTGTTTGGCATTTTGGCACACAT 240
QY 241 GTGTGACGCTGGTATTTAAGCCGAGTGAAGCAGGAGGTCTCCATTTTGAAGCGGGA 300
Db 241 GTGTGACGCTGGTATTTAAGCCGAGTGAAGCAGGAGGTCTCCATTTTGAAGCGGGA 300
QY 301 GGTTTGAACGGCGAG-CGCCATGCGGGGTTTACGAGATTGATTAAGTCCCGAGCG 359
Db 301 GGTTTGAACGGCGAGCGGCGCATGCGGGGTTTACGAGATTGATTAAGTCCCGAGCG 360
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QY	360	ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAACCTGGGTGGCCGAGAAAG	419
Db	361	ACCTTGAACGGGATCTGGCCCGGCATTTCTGACAGCTTTGTGAACCTGGGTGGCCGAGAAAG	420
QY	420	AATGGAGTGTGCGCGACAGATTCTGACATGAGATCTGAAATCTGAAATTGAGATGGGACCCCTGA	479
Db	421	AATGGAGTGTGCGCGACAGATTCTGACATGAGATCTGAAATCTGAAATTGAGATGGGACCCCTGA	480
QY	480	CCGTGGCCGAGAAAGCTGACGCGCATCTTCTGGTCCACTGGCGCCGCGTGAATGAAGCCC	539
Db	481	CCGTGGCCGAGAAAGCTGACGCGCATCTTCTGACGGAATGGCGCGGTGTGAATGAAGGCC	540
QY	540	CGGAAAGCCCTCTTTTGTGTCAGTTGTGAGAAAGGCGAGTCTCACTTCCACTTCATATTC	599
Db	541	CGGAAAGCCCTTTTGTGTCAGTTGTGAAGAGAGAGACTTATTCACATGACAGTGC	600
QY	600	TGGTGGAGACACACGGGGGTCAAATCCATGGTCTGGGCGCTTCCTGAATCAGATTAGCG	659
Db	601	TGTTGGAAACCAACCGGGGTGAATTCATGGTTTGGGAAGTTTCTTGATCAGATTCCGCG	660
QY	660	ACACGCTGGTGACAGCCATCTACCGCGGGATGAGCCGACCCCTGCCAATCTGTTTCGCG	719
Db	661	AAAACTGATTCAAGAAATTTACCGGGGATCGAGCCGACTTTGCCAACTGGTTCGCGG	720
QY	720	TGACCAAGCGGTTAATGCGCGCGGAGAGGGGGGAAACAAGTGGTGGACAAGATCTCAATCC	779
Db	721	TCACAAAGACCAAAATAGCGCGGAGGGGGGAAACAAGTGGTGGATGATGATCTACATCC	780
QY	780	CCAACTACCTCTGCGCCCAAGACTACGCGGACCTGATGGCGCTGACATACATGAGAG	839
Db	781	CCAAATTACTTGCTCCCAAAAACCAAGCCTGAGCTCAAGTGGCGTGAATATATGAGAAC	840
QY	840	AGTATATAAGCGCGGTTTAAACCTGGCGGAGCGCAAAAGGCTCGTGGCGCACAGACTGA	899
Db	841	AGTATTTAAGCGCGCTGTTGAATCTCACGGAACGTGAACGGTTGGTGGCGACATCTGA	900
QY	900	CCCAAGTCAGCCAGACCCGAGAGCAAGAACAAAGAAATCTGAAACCCCAATTTGACGCGC	959
Db	901	CGCACTGTGCGGAGACGAGAGCAAGAACAAAGAAATCTGAATCCCAATTTGATGGCG	960
QY	960	CTGTATATCCGGTCGTAATAAACCTTCCGACGCTACATGAGCTGGTGGGTGGCTGTGAGACC	1015
Db	961	CGGTATACAGATCAAAAACCTTACGCGAGTTACATGAGCTGGTGGGTGGCTGTGAGACA	1020
QY	1020	GGGGATCACTCCGAGAAAGCATGAGATCTCAGAGAGAACGAGGCGTCGATCAATCTCCTTCA	1079
Db	1021	AGGGATTAACCTCGAGAAAGCATGAGATCTCAGAGAGAACGAGGCGTCATATCAATCTCTTCA	1080
QY	1080	ACGCGGCTCCAACTCGCGGTCCAGATCAAGACGCGCTCTGGAACATGCCGCAAGATCA	1139
Db	1081	ATGCGGCTCCAACTCGCGGTCCCAATCAAGCTGCTTGGACATGCGGGAAAGATTAA	1140
QY	1140	TGGGCTGACAAATCCGCGCGCCGACCTACCTGTGAGGCCCGGCTCGCGCCGACATTA	1199
Db	1141	TGAGCTTACTTAAACCGCGCCCGACCTACCTGTGAGGCCCGACGCGCTGTGAGACATTT	1200
QY	1200	AAACCAACCGCATTTACCGCATCTCTGAGCTGAAGCGGCTACGACCCCTGCTACGCGGCT	1258
Db	1201	CCAGCAATCGGATTTATTAATAATTTTGGAACTTAAACGGGTACGATCCCAATATGGGCTT	1260
QY	1260	CCGTCTTTCTCGGCTGGGCGCCAGAAAAGGTTGGAAAAACGCAACCACTTGGCTGTTTG	1319
Db	1261	CCGTCTTTCTGGGAGGGGCAACGAAAAAGTTTCGCGAAGGAAACCACTTGGCTGTTTG	1320
QY	1320	GGCGCGGACCAACGGGCAAGAACCAACATCGCGGAAGCATCGGCCACGCGCGCTCTCT	1379
Db	1321	GGCTCTGACATACCGGAAAGCAACATCGCGGAAGCCATAGCCCACTGTGCCCTTCT	1380
QY	1380	ACGGCTGCGTCAACTGAGACCAATGAACTTTCCTTCAAGATTCGTCGTGACAGATGG	1439
Db	1381	ACGGGTGGTAACTGAGACCAATGAACTTTCCTTCAAGATTCGTCGTGACAGATGG	1440

QY	1440	TGATCTGGTGGAGAGGCAAGATGACGGCCAAAGCTGTGGAGTCCGCAAGGCCATTCC	1498
Db	1441	TGATCTGGTGGAGAGGAGGAAGATGACCGCCAAAGCTGTGGAGTCCGCAAGGCCATTCC	1500
QY	1500	TGGGGGGAGCAAGGTTGGCGGTGGAGCAAAAAGTGCAGTCGCGCCAGATCGATCCCA	155
Db	1501	TGGAGAGAGCAAGGTTGGCGGTGGAGCAAAAAGTGCAGTCCTCGGCCAGATGAGCCGA	156
QY	1560	CCCCCGTATCGTCACTTCCCAACCAACATGTGGCCGTGATTGACGGGAACAGCACCA	161
Db	1561	CTCCCGTATCGTCACTTCCCAACCAACATGTGGCCGTGATTGACGGGAACCTCAAGCA	162
QY	1620	CCTTGAGCAACCAAGCCGTTTGACAGACCGGATGTTCAAAATTGAACTCACCCCGCTC	167
Db	1621	CCTTGAAACACCAAGCAGCCGTTTGCAAGACCGGATGTTCAAAATTGAACTCACCCCGCTC	168
QY	1680	TGGACATGACTTTTGGCAAGTGCACAAAGCAGAAAGTCAAAAGTCTTCCGTGGGGCG	173
Db	1681	TGGATCAATGACTTTTGGGAAGTGCACCAAGCAGAAAGTCAAAAGCTTTTCCGTGGGGCA	174
QY	1740	AGGATCACTGTGACCAAGGTGGCGGCTGAGTTCTTACGTACAGAAAAGGTTGAGCCAAACA	179
Db	1741	AGGATCACTGTGTTGAGGTGGAGCTGAAATTTCTACGTCAAAAAGGTTGAGCCAAAGAAA	180
QY	1800	GACCCGCCCCCGATGACCGGATTAATAAGCAGGCCCAAGCCGGCGCTCCCTCAGTCGCGG	185
Db	1801	GACCCGCCCCCGATGACCGAGTATTAATGAGCCCAAGCCGGGTGCGAGTCAGTTGGCG	186
QY	1860	ATCCATCGACGTCAAGCCGCGAAGAGGCTCCGTTGACTTTGGCAGACGTACCAAAACA	191
Db	1861	AGCCATTCACGTCAACCGCGA---AGCTTGATCTACATTAAGCACAACAGTACCAAAACA	191
QY	1920	AATGTTCTCGTACCGCGGAGATGCTTGAGATGCTTTCCGTGCAAAAATGCGCAGAGAA	197
Db	1918	AATGTTCTCGTACCGTGGCAGTGAATCTGAATGCTTTTCCGTGCAACAATGCGCAGAGAA	197
QY	1980	TGAATCAGAAATTCAAACATTTGCTTACGCAACGGGACAGAGACTGTTCAAGATGTTTCC	203
Db	1978	TGAATCAGAAATTCAAATATCTGCTTCACTACCGGACAGAAAGACTGTTTAGAGTCTTTC	203
QY	2040	CCGGGCTGTCAAGATCTAACCCGCT---CGTCAAGAAAGAGACGTATGCGAACTCTGTG	209
Db	2038	C---CGTGTCAAGAACTCTCAACCCGTTTCTGTCTCAAAAAGCGTATCAGAAACTGTCTCT	209
QY	2097	CCATTTCATCTGTGTGGGGGGGGCTCCGAGATTGCTGTGCTCGGCCCTGCAATCTGCTCA	215
Db	2095	ACATTCATCAATATCAATGGGAAAGGTCGAGA---CGTGTGACCTGCTGCAATCTGCTCA	215
QY	2157	ACGTGATCTGTGATGACTGTGTTTCTGAGCAATAAATGACTTTAAACAGATATGGCTCC	221
Db	2152	ATGTGATTTTGGATGATGTCATCTTTGAAACAATTAATTAATTTAAATCAAGTATGGCTCC	221
QY	2217	GATGTTATCTTCAGATTGGCTCGAGGACAACTTCTGAGGGCAATTCGCACTGTGG	227
Db	2212	GATGTTATCTTCAGATTGGCTCGAGGACACTCTCTGAAAGGAATTAAGACAGTGTGG	227
QY	2277	GACTTGAAACTGTGAGCCCCCGAAACCCAAAGCCACAGCAAGCAAAAGCAGAGACGACCGG	233
Db	2272	AACTCAAACTGTGGCCCAACCAACCAAAAGCCGACAGCGGCAATTAAGAGACACAGCAGG	233
QY	2337	GGTCTGAGTCTTCCTGAGCTACAGATGACTCGGACCTTCAACCGGACTGCAAGAGGGAG	239
Db	2332	GGTCTGAGTCTTCCTGAGTACAGATGACTCGGACCTTCAACCGGACTGCAAGAGGGAG	239
QY	2397	CCGCTCAACGCGGCGGATGACGCGGCTCTGAGACGACAGAGGCTTACGACCAAGCTC	245
Db	2392	CCGCTCAACGAGGACGACGCGGCTCTGAGACGACAGCAAAAGCTTACGACCGGCAAGCTC	245
QY	2457	AAAGCGGTGCAATTCGTAATCTGCGGTATTAACAAGCCGACGCGCGATTTCAAGAGCT	251
Db	2452	GACAGCGGAGCAACCGGTACTTAAGTACAACAACGCGCAGCGGAGTTTCAAGAGGCG	251
QY	2517	CTGCAAGAAATACGTCTTTTGGGGGGCAACTCGGGGAGAGAGTCTTCCAGGCCCAAGAG	257

Db	2512	CTTAAAGAGATACCTCTTTGGGGGCAACCTCGAGCAGACGCTTCTCAAGCGAATAAG	25711
Oy	2577	AGGGTTCTCGAAACCTTTTGTCTGGTTAGGAAGGTGCTAAGACGGCTCTCTGGAAGAA	2636
Db	2572	AGGGTCTTTGAACCTCTGGGCGTGGTTAGGAACCTGTTAAGAAGGCTCCGGGAAAAAG	26311
Oy	2637	CGTCCGGTAGAGCACTGCCACAGAGCCAGACTCTCTCTGGGGCATTTGGCAAGCAGGC	2686
Db	2632	AGGCCGGTAGAGCACTCTCTGTGGAGCAAGACTCTCTCTGGGAAACGGAAAGCGGGC	26911
Oy	2697	CAGCAGCCCGCTAAAGAAGACTCAATTTGGTTCAGCTGGCGACTCAGAGTCACTCCC	2756
Db	2692	CAGCAGCTTCGAAGAAAAAGATTGAATTTTGGTCAGCTGGAGACGAGACTCACTACT	27511
Oy	2757	GACCCCAACCTCTCGAGAACTCTCAGCAACCCCCGCTGCTGGGACCTACTCAATG	2816
Db	2752	GACCCCGAGCTCTCGAGCAGCAACAGACGCCCTCTGGTCTGGGAATCAATACGATG	28111
Oy	2817	GCTTCAGGGGGGGGCGACCAATGGCACAATAAGAAAGGGCGGACGGAGTGGGTAT	2876
Db	2812	GCTACAGGCGAGGGGCAACCAATGGCACAATAAGAGGGGGCCGACGGAGTGGGTAT	28711
Oy	2877	GCCTCAGGAAATTGGCATTTGGCATTTCCACATGGCTGGGCGACAGAGTCATCAACAGC	2936
Db	2872	TCCTCGGAATTTGGCATTTGGCATTTCCACATGGAGTGGGACAGAGTCATCAACAGC	29311
Oy	2937	ACCCGAACATGGGCTTGGCCCACTATAACAACCACTCTACAGCAATCTCAGTCT	2996
Db	2932	ACCCGAACCTGGGCTTGGCCCACTATAACAACCACTCTACAAATTTCCAGCCAA	29911
Oy	2997	TCAAAGGGGGCCAGACAAGACAACACACTTCGCTACAGCACCCCTGGGGGATATTT	3056
Db	2992	TCA---GGAAGCTCGAAGCAGATACACTACTTTGGCTAAGACACCCTTTGGGGGATTTT	3048
Oy	3057	GATTTCAACAGATTTCACTGCCATTTTCTCAACAGTACCTGGCAGCGACTATCAACAC	3116
Db	3049	GACTTCAACAGATTTCACTGCCACTTTTTCACCACTGACCTGGCAAGACTCATCAACAC	3108
Oy	3117	AATTGGGAATTCGGGCCCAAGAGACTCAACTCAGACTCTTCAATCAAGTCAAGAG	3176
Db	3109	AAGTGGGAATTTCCGACCCAGAGACTCAACTTCAGACTTTTACATTCAGGTCAAGAG	3168
Oy	3177	GTCAAGACGAATGATGGCGTCCAGACATCGCTAAATACCTTTACAGACGGTTCAGTC	3236
Db	3169	GTCAAGCAGAAATGACGTATCGACGACGATGGCCAAATACCTTACAGACGGTTCAGTG	3228
Oy	3237	TTGTGGGACTCGGAATACAGTTCCCGATACGTCCTCGGCTCGGCCACAGAGGCTGCTC	3296
Db	3229	TTTACTGACTCGGAATACAGTCTCCGATCGTCCTCGGCTCGGCCCATCAAGAGTCTC	3288
Oy	3297	CTTCGTTCCCGGCGGACGATGTTCAATGATTCGCGAGTACGCGTACCTAACGCTCAACAT	3356
Db	3289	CCGCCGTTCCAGACGAGCGTCTTACATGGTCCACAGTATGATTACTCACCTGAAACAC	3348
Oy	3357	GGCAGCCAGGCAGTGGGACGCTCATCTTTTACCTGCGTGGAAATATTTCCATCGAGATG	3416
Db	3349	GGGAATCAGGCGATGGAGCGCTCTTCATTTTATCTCCTGGAGTACTTTCCTTCCAGATG	3408
Oy	3417	CTGACAAAGGCAATTAACCTTACCTTCAGCTACACTTCGAGAGCGTGCCTTTCACAGC	3476
Db	3409	CTGCGTACCGGAAACAACTTTTACCTTCAGCTACACTTTTGAAGAGCTTTCCTTTCACAGC	3466
Oy	3477	AGCTACGGGACAGCCAGACGCTGGAACGGGCGATGAATCTCTCATGACCAATGCTG	3536
Db	3469	AGCTACGCTCACAGCCAGAGTGTGACCGGCTCATGAATCTCTCATGACCAATGCTG	3528
Oy	3537	TATTACCTGAACAGAACTACAAATAGTCCGGAATGCCCAAAACAAGACTTGTGTTT	3596
Db	3529	TATTACTTGAAGCAAAACACTCCAAAGTGAACCAACAGCACTCAAGGCTTAAGTTT	3586
Oy	3597	AGCCGTGGGTCTCCAGCTGGCACTGTTCTTTCAGCCCAAAACCTGGCTACCTGACCTGT	3656

Db	3589	ICTGAGCGCCGAGGAGTGAACATTTCGGGACCAAGTCTTAGAACTGGCTTCCTGGACCTGT	3648
Qy	3657	TACCGGACGACGCGGTTTCTTAAACAAAAAGACAAACAACAACAGACTTTACTCTGG	3716
Db	3649	TACGGCCACGACGCAAGTATCAAAACACTCTGCGATTAACAACAACACTGTAATCTCTGG	3708
Qy	3717	ACTGGTGTTCAAAATATTAACCTTAATGGGCGGTAAATCTATTAATCAACCTGGACCTGT	3776
Db	3709	ACTGAGCTTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTAATTCGGGCGCCGC	3768
Qy	3777	ATGGCTTCACAACAAGACGAACAAGATCTTTTCCATGACCGGTGCATGATTTT	3836
Db	3769	ATGGCAACCCACAAGACGATGAAGAAAAGTTTTCCTCGAGACGGGAGTTCATCTTT	3828
Qy	3837	GGAAAGGAGACGCGCGAGCTTCAACACCTGCATTGGAACAATGATATGATCACAGCA	3896
Db	3829	GGGAAGCAGGCTCAGAGAAAACAAATGTGACAATGAAGATGATATTAACAGACGA	3888
Qy	3897	GAGCAATCAAGCCACTTAACCCCGTGGCCACCGAAAGATTTTGGACTGTGGACGTCAAT	3956
Db	3889	GAGGAATTCGGAACAACCAATCCGTGGCTATCGAGCGATATGTTCTGATCTTACCAAC	3948
Qy	3957	CTCCAGACAGCAGACAGACCCCTGCGACCGGAATGTGATGTTATGGGAGCTTACCT	4016
Db	3949	CTCCAGAGGCAACAGACAAGACGCTACCGCAATGTCAACACAGAAGGTCCTTCA	4008
Qy	4017	GGAAATGTGTGGACAGAGACAGATATACCTGTGAGGAGTCTTATTTGGCCAAATTCCT	4076
Db	4009	GGCATGTCTGGCAGACAGACAGATGTGTACTCTTAAGGGGCCCATCTGGCAAGATTCA	4068
Qy	4077	CACACGATGACACTTACCCCGTCTCTCTCAATGGCGGCTTTGACTTAAGACCCG	4136
Db	4069	CACACGGACGCAATTTTCACCCTCTCCCTCAATGGGTGGATTTCGACTTAAACACCT	4128
Qy	4137	CCTCCTCAGATCCATATAAAACAGCGCTGTCTGCGAATCCTCCGGCAGATTTTCG	4196
Db	4129	CCTCACAAGATTCATTAAGAAACACCCCGTACTGTGGAATCTTTGACCACTTCAGT	4188
Qy	4197	GCTACAAAGTTTGCTTCAATTCATCACCCAGATTCCAAGAGCA-AGTGAACGTGAGAT	4255
Db	4189	GGGGCAAGTTTGCTTCCTTCATCACACAGTACTCAAGGGAACAGCGTACGCGGAGAT	4248
Qy	4256	TGAATGGAGCTGCAGAAAAGAAAACAGAAACGCTGGAATCCGGAATGCAGTATACATC	4315
Db	4249	CGAGGGGAGCTGCAGAAAGAAAACAGAAACGCTGGAATCCGAAATTCAGTACATTC	4308
Qy	4316	TAACTATCAAAATCTGCCAACGTTGATTTACTGTGGAACAACAATGACTTTTACTGA	4375
Db	4309	CACACTCAACAAGTCTGTTAATCGTGAACCTTACCCTGGATCTTAATGGCGTGAATTCAGA	4368
Qy	4376	GGCTGCGCCATTTGGACCCGTTACCTACCCGTCCTCTGAATTTGTGTTAATCAATA	4435
Db	4369	GGCTGCGCCCATTTGGCACCAATACCTGAATCTGTAATGTGTGTTAATCAATA	4428
Qy	4436	AACCGGTTAATTCGTGTAGTTGAATTTGGTTCATGTCCTTAATTTCTATATGTCGA	4495
Db	4429	AACCGTTAATTCGTGTAGTTGAATTTGGTCTCTGTGATTTCTTCTTATCTAAGTTT	4488
Qy	4496	CCATAGCAACCGGTTACATTAATCTGTTAGTTCGGCTTGCGA----ATACCCTAGT	4551
Db	4489	CCATGGCTACGTAAGATTAATTAGCATGGCGGGTTATCATTAATCAAGAACCCCTAGT	4548
Qy	4552	GATGAGATTGCCACTCCCTCTATATGCGGCTCGCTCGTCCGTGGGGCCGGCAAGAGA	4611
Db	4549	GATGAGATTGGCACTCCCTCTCTGCGGCTCGCTGCTCACTAGGCGGGGCAACAAA	4608
Qy	4612	GCTTGCAGTTCGCGACCTTTGGTCGACAGGCCCAACCGAGCAGACGCGCCATAGA	4671
Db	4609	GGTCCCGGACCCCGGGCTTTGCCCGGCGGCTCAAGTAGCAGAGCGAGCGCGAAGA	4666
Qy	4672	GGAGGTGCGCAA 4683	
Db	4669	GGAGGTGCGCAA 4680	

RESULT 9

PCT-US95-07178-1

Sequence 1, Application PC/TUS9507178

GENERAL INFORMATION:

APPLICANT: Johnson, Philip R.

TITLE OF INVENTION: Adeno-Associated Virus Materials and

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07178

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31975

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4680 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-07178-1

Query Match 69.8%; Score 3270.8; DB 7; Length 4680;
 Best Local Similarity 82.2%; Pred. No. 0; Mismatches 812; Indels 21; Gaps 8;
 Matches 3859; Conservative 0;

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QY 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGCCGGGCGCAAAAGTCCG 60
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DB 61 CGAGCGCCGGGCTTTGCCCGGGCGGCTCACTGAGCGAGCGCGCGAGAGGAGTG 120
QY 121 GCCAACTCCATCTAGAGGTTCTGAGAGGGGTGAGTGTGAGTGAATTAAGTCAATAG 180
DB 121 GCCAACTCCATCTAGAGGTTCTGAGAGGGGTGAGTGTGAGTGAATTAAGTCAATAG 180
QY 181 GGTTAGGAGAGTCTGTATTAGAGGTCACTGAGTGTGTTGCGACATTTTGCGACCAT 240
DB 181 GGTTAGGAGAGTCTGTATTAGAGGTCACTGAGTGTGTTGCGACATTTTGCGACCAT 240
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QY 301 GGTTAGGAGCGAG-CGCCATGCGGGGTTTACGAGATTGTGATTAAGTCCCGAGCG 359
DB 301 GGTTAGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 360 ACCTTAGCAGAGCATCTGCGCGGCAATTTCTGACAGCTTTGTGAATGAGTGGCGGAGAG 419
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DB 901 CCAAGTCAAGCAGACCCAGAGCAGAACTGAACTGAACTGAACTGAACTGAACTGAACT 960
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DB 1081 ATGCGGCTCCCACTCGCGGTCCAGATCAAGGCGCTGTGAGCAATGCGGCAAGATCA 1140
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DB 1141 TGGCGCTGACCAATTCGCGCGCGGACTTACTGTGAGGCGCGCGCTGCGCGCGGACTTCA 1200
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DB 3469 AGCTACGCTCAACGCGAGCTTGAACCGGCTGATGATCTTCTCATGACAGATACCTG 3528
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Qy 4137 CCTCTCATGATCTTATCAAAAACGCTGTCTCTGGAATCTTCGGCAGAGTTTTCG 4196
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Qy 4197 GCTACAAAGTTTGTCTTCAATTCACCCAGTATTCACAGACA -AGTAGCGTGAAT 4255
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Db 4249 CGAGTGGAGCTGCAGAAAGAAACAGCAACGCTGGAATCCGAAATGCAATATC 4308
Qy 4316 TAACTATGCAAAATTCGCCAAGTTGATTTCACTGTGACAAACATGACTTTAATCTGA 4375
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RESULT 10

US-09-807-802A-18
; Sequence 18, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNPV. 03USA
; CURRENT FILING DATE: US/09/807, 802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 4681
; TYPE: DNA
; ORGANISM: AAV-2
US-09-807-802A-18
Query Match 69.8%; Score 3267.8; DB 3; Length 4681;
Best Local Similarity 82.3%; Pred. No. 0;
Matches 3864; Conservative 0; Mismatches 807; Indels 22; Gaps 9;
Qy 1 TTGGCACTCCCTCTGCGGCTGCTGCTCACTGAGCGCGGACCAAGGTGCGC 60
Db 1 TTGGCACTCCCTCTGCGGCTGCTGCTCACTGAGCGCGGACCAAGGTGCGC 60
Qy 61 CGAGCCCGGGCTTGGCCCGGGCGGCTCACTGAGCGAGCGGCGGAGGAGGAGTG 120
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RESULT 11
 US-09-782-378A-1
 ; Sequence 1, Application US/09782378A
 ; Patent No. 6916635
 ; GENERAL INFORMATION:
 ; APPLICANT: Hearing, Patrick
 ; APPLICANT: Bahou, Wadie
 ; APPLICANT: Sandelon, Ziv
 ; APPLICANT: Gnatenko, Dmitri
 ; TITLE OF INVENTION: Adenoviral Vectors
 ; FILE REFERENCE: STONTB-04970
 ; CURRENT APPLICATION NUMBER: US/09/782,378A
 ; PRIOR FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/237,747
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 4675
 ; TYPE: DNA
 ; ORGANISM: Human adeno-associated virus 2

US-09-782-378A-1

69.3%; Score 3244.2; DB 3; Length 4675;

Query Match 82.2%; Pred. No. 0; Mismatches 808; Indels 28; Gaps 10;

Best Local Similarity 0; Conservative 0; Matches 3857;

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Db 3169 GGTCAAGCAAGATGACGGTACAGACGATTTGCCAATAACCTTACACACGTTCAAGT 3228
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Qy 4611 AGCTTCCTGCTGTCGGAAGCTTTGGTTCGCAAGCCCAACGAGCGAGCGAGCGCATAG 4670
Db 4603 AGGTCGCCCCGACGCGCGGGCTTTGCCCGGGCGGCTCAGTAGCGAGCGAGCGCAGAG 4662
Qy 4671 AGGAGTGGCCAA 4683
Db 4663 AGGAGTGGCCAA 4675

RESULT 12

US-09-782-378A-2

Sequence 2, Application US/09782378A

Patent No. 6916635

GENERAL INFORMATION:

APPLICANT: Hearing, Patrick

APPLICANT: Bahou, Madie

APPLICANT: Sandaou, Ziv

APPLICANT: Gatenko, Dmitri

TITLE OF INVENTION: Adenoviral Vectors

FILE REFERENCE: STONYB-04970

CURRENT APPLICATION NUMBER: US/09/782.378A

CURRENT FILING DATE: 2001-02-12

PRIOR APPLICATION NUMBER: 60/237,747

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 4675

TYPE: DNA

ORGANISM: Human adeno-associated virus 2

US-09-782-378A-2

Query Match 69.3%; Score 3244.2; DB 3; Length 4675;

Best Local Similarity 82.2%; Pred. No. 0;

Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

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Db 361 ACCTTGACGCGCATCTGCCCCGCGATTTCTGACAGCTTTGTGAATCTGGGTGCGGAAGG 420
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Qy 600 TGGTGGAGACCAAGGGGTCATATCCATGCTGGGCGCTTCTGAGTCAATTAAGCG 659
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Qy 660 ACAAGCTGTGACAGACCATCTACCGGGATCGAGCCGACCTTGCCCATGTTGCGG 719
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Qy 720 TGAACCAAGACGCTAATGCGCGGAGCGGGGGAACAAGGTGTGGAAGAGTGTACATCC 779
Db 721 TGAACCAAGACGCTAATGCGCGGAGCGGGGGAACAAGGTGTGGAAGAGTGTACATCC 780
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Db 781 CCAACTACTCTCTGCGCAAGACTCAGCCGAGCTGAGTGGGCGTGAATCATGAGAG 840
Qy 840 AGTATTAAGCGCGTGTAACTCTGGCGAGCGCAACGCGTGTGGCGCAGCAGCTGA 899
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Qy 1320 GCGCGGCAACGCGGCAAGACCAATCGCGGAAGCCATCGCCGCGCTGCTCT 1379
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4663 AGGAGTGGCCAA 4675
RESULT 13
us-10-111-708-1
; Sequence 1, Application us/10111708
; Patent NO. 6995010
; GENERAL INFORMATION:
; APPLICANT: UENO, Takashi
; APPLICANT: MATSUMURA, Hajime
; APPLICANT: TANAKA, Kei-ji
; APPLICANT: IWASAKI, Tomoko
; APPLICANT: UENO, Mitsuhiko
; APPLICANT: FUJINAGA, Kei
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: GENE TRANSFER METHOD
; FILE REFERENCE: UENO=9
; CURRENT APPLICATION NUMBER: us/10/111,708
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: PCT JP00 07373
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: JP 11/308839
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4675
; TYPE: DNA
; ORGANISM: Adeno-associated Virus
us-10-111-708-1
Query Match 69 3%; Score 3244.2; DB 4; Length 4675;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;
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361 ACCTTGACGCGCATCTGCGCGCATTTCTGACAGCTTTGTGAACGAGTGGCGCGAGAGG 420
420 AATGGAGTTGGCGCGAGATTTCTGACATGATTTGATTTGATTTGACAGGACCCCTGA 479

Dh 421 AATGGAGTTCGCCGACAGATTCCTGACATGATCTGAATCTGATGAGCAGGACCCCTGTA 480
Qy 480 CCGTGGCCGAGAAAGTTGAGCGCGA CTTCCGTGCTCACTGCGCGCCGCTGATAGGCCC 539
Db 481 CCGTGGCCGAGAAAGTTGAGCGCGA CTTCTGACGAAATGCGCGGTGAGTAAGGCC 540
Qy 540 CGSAGGCCCTCTTCTTGTTCAGTTGAGAAAGGCGAGTCTTACTTCCACCTCCATATTC 599
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Qy 600 TGTGTGAGACCA CGGGGGTCAATCATGTGCTGCGCGCTTCTGATCAGATTAGCG 659
Db 601 TGTGTGAGAACCA CGGGGGTGAATCATGTGTTTGGGAGTTTCTGATCAGATTCCG 660
Qy 660 ACAAGCTGTGAGACCATCTAACCGCGGGATGAGACCCGCTGCCAATGTTTCCGG 719
Db 661 AAAAACTATTTCAGAAATTTTACCGCGGGATGAGCCCATTTGCAAACTGGTTCCGG 720
Qy 720 TGACCAAGACGCTAATGCGCGCGAGGGGGAA CAAGTGTGAGACGATGCTCATCC 779
Db 721 TCACAAAGACCAAGAAATGGCCCGAGGCGGGAA CAAGTGTGAGATGATGCTCATCC 780
Qy 780 CCAACTACCTCTGCTCCAGAACTCAGCCGAGCTGAGTGGCGTGA CTAAATGAGAG 839
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Qy 840 AGTATATAAGCGCGTGTAAACCTGCGCGAGCGCAACCGCTGCTGGCGCACGCTGA 899
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Qy 900 CCCACGAGCGCAGACCCAGAGCAGAA CAAGGAATCTGAACCCCAATCTGACGCGC 959
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Qy 960 CTGTGATCCGGTCAAAAACTTCCGCACTCATGAGCTGGTGGGTGCTGTGTAAC 1019
Db 961 CGGTGATCAGATCAAAAACTTCAAGCAGGTGACATGAGACTGGTGGGTGCTGTGTAAC 1020
Qy 1020 GGGGCTACCTCCGAGAAAGATGATTCAGAGAGACCAAGGCTCTGATCATCTCTTCA 1079
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Qy 1080 ACGCGGCTCCAACTCGCGGTCCCGATCAAGGCGCTCTGGA CAATGCGGCAAGATCA 1139
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Qy 1200 AAACCAACCGCATTTACCGCATCTGTGAGCTGAACGCTACGCTTACGCGGCT 1259
Db 1201 CCACCAATCGGATTTATTTAAATTTTGAATTAACGAGTACGATCCCAATATGCGGCTT 1260
Qy 1260 CCGCTTTCTCGGCTGGGCGCCAGAAAAGTTCCGAAAAAGCAACCACTGCTGTTT 1319
Db 1261 CCGCTTTCTCGGCTGGGCGCCAGAAAAGTTCCGAAAAAGCAACCACTGCTGTTT 1320
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Qy 1380 ACGGCTGCTCACTGAGCAATGAGAACTTTCCCTTCAAGATTGCTGCAAGATG 1439
Db 1381 ACGGCTGCTCACTGAGCAATGAGAACTTTCCCTTCAAGACTGTGCAAGATG 1440
Qy 1440 TGAATCTGTGAGAGAGGCAAGATGAGCGCAAGGCTGTGAGTCCGCAAGGCAATTC 1499
Db 1441 TGAATCTGTGAGAGAGGCAAGATGAGCGCAAGGCTGTGAGTCCGCAAGGCAATTC 1500
Qy 1500 TCGGCGCAGCAAGGTGCGCTGGAACCAAAAGTCAAGTCTGCGCCAGATTCGATCCA 1559
Db 1501 TCGGAGGAAGCAAGGTGCGCTGGAACCAAAATGCAATGCTCGGCGCAAGATGAGCCGA 1560

Qy 1560 CCCCCTGATGCTGACCTCCAAACA CAATGTGGCGCGTGAATTTGAGCGGAAACAGACCA 1619
Db 1561 CTCCGATGATGACCTCCAAACACCAATGTGGCGCGTGAATTTGAGCGGAACTCAACGA 1620
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Db 1621 CTTTGAAGCACACAGCCGTTGAGAGACCGGATGTTCAAAATTTGAATCTCACCCGCTC 1680
Qy 1680 TGAAGCATGACTTTGGCAAGGTGACAAAGCAAGAAAGTCAAAAGATTCTTCCGCTGGCGC 1739
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Qy 1920 AATGTTCTCGTACAGCGCGGCAATGCTTCAAGTCTGTTCCCTGAAACATGCGAGAA 1979
Db 1918 AATGTTCTCGTACAGCGCGGCAATGATGATGCTGTTTCCCTGAAACATGCGAGAA 1977
Qy 1980 TGAATCAGAAATTTCAACATTTGCTTCAAGCAGCGGACAGAGACTGTTCAAGATGTTCC 2039
Db 1978 TGAATCAGAAATTTCAAAATTCGCTTCACTACGAGCAAGAAAGATGTTTAAAGTCTTTC 2037
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Db 2038 C---CGTGTCAAGATCTCAACCGGTCTGTGCTGCTCAAAAGAGCGCTATCAGAAATGTGCT 2094
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Db 2095 ACATTCATCATATCATGGAAGAGGTGCCAG--CGCTGACATGCTGCGATCTGCA 2151
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Db 2152 ATGTGAATTTGAGTACTGATCTTTGACAAATTAATGATTTAAATCAGATATGCTGCC 2211
Qy 2217 GATGTTATCTTCAAGATTTGCTGAGAGCAACTCTCTGAGGCAATTCGCGAGTGTG 2276
Db 2212 GATGTTATCTTCAAGATTTGCTGAGAGCACTCTCTGAGGAAATTAAGACAGTGTG 2271
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Db 2272 AAGCTCAAACTGCGCCCAACCAACCAAGGCCGAGCGGCAATTAAGAGAGAGAGCG 2331
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Db 2332 GGTCTGTGCTTCTGTGCTACAATGACTCGGACCTTTCACAGGACTGACAAAGGAGAG 2391
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Db 2392 CCGGTCAACCGGAGAGAGCGCGCGGCTTGAAGACGATCAAAAGCTTACGACAGAGCT 2451
Qy 2456 CAAGCGGAGAGCAATCGTATCTGCGGTATTAACAAGCGGCGGAGTTTCAAGAGCG 2515
Db 2452 CGAAGCGGAGAGCAACCGTATCTCAAGTATCAACACAGCGGAGCGGAGTTTCAAGAGCG 2511
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Db 2512 CTTTAAAGAAAGTACGTTTGTGGGCAACTTGGGCGAGAGTCTTTCAGGCGCAAGAA 2571
Qy 2576 GAGGTTCTGAACTTTTGTGTTGTTGAGAGAGGTGCTTAAGCGGCTCTTGAAAGAA 2635
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OY	3776	TATGGCCTCAACAAGAAGCAAAAGCAAGTTCTTTTCCATGAGCGGTGCATGATTTT	3835
Db	3763	CATGGCAAGCCACAAGAGCAGATGAAGAAAGTTTCTTCAGAGCGGGGTTCATCTT	3822
OY	3836	TGGAAAGAGAGCGCCCGAGCTTCAACACTGCACTTGGACAATGTCAATGATTCACAGACGA	3895
Db	3823	TGGGAACAAGGCTCCACAGAAAAAATAATGTGAACATTGAAAAGGTCATGATTAACAGACGA	3882
OY	3896	AGAGGAATATCAAAAGCCACTAAACCCCTGTGGCCACCGAAGATTTGGGACTGTGGCAGTCAA	3955
Db	3883	AGAGGAATATGGGAACAACCAATCCCGTGGCTACGGAGCAGATGTCTTGATCTACAA	3942
OY	3956	TTCTCAAGACAGCAGCACAAGCCTGGGACCGGAGATGTGCATGTTATGGAGCCTTACC	4015
Db	3943	CTTCACAAGAGGCAACAGACAAAGAGTTACCGCAGAGTCAACACACAAAGCGTTCTCC	4002
OY	4016	TGGAATGATGTGGCAAGACAGAGCAATATACCTTCAGAGGTCTCTATTTGGGCAAAATTC	4075
Db	4003	AGGCAATGTCTGGCAGAGCAGAGATGTGTACTTCAAGGGGCCAATCTGGGCAAAAGATTCC	4062
OY	4076	TCACACGAGTGAACACTTTCAACCCGCTCTCTCTCATGGCGGCTTTGACTTAAGCACCC	4135
Db	4063	ACACACGGAGCGGAATTTTCAACCCCTCTCCCTCATGGTGGATTCGACCTTAAACACC	4122
OY	4136	GGCTTCCTCAGATCCTCATCAAAAACAGCGCTGTCTCGGCAATCTCCGGCAGAGTTTTC	4195
Db	4123	TCCTTCACAGATTTCTCATCAAGAACACCCGGTACTCTGCAATCTTTCGACCACTTCAG	4182
OY	4196	GGCTCAAAAGTTTGCTTCATTTCATCACCAAGTATTTCCACAGACA-AGTAGCGTGGAGA	4254
Db	4183	TGCGGCAAAAGTTTGCTTCCTTCATCAACAGTATTCACGGGACACGGTCAACCTGGAGA	4242
OY	4255	TTGAAATGGAGACTCCAGAAAGAAAACAGCAAAGCTGTGAATCCCGAAGTGCAGATATCAT	4314
Db	4243	TCGATGGGAGCTCCAGAAAGGAAAAACGAAAGCCTGGAATCCGAAATTCAGTACACTT	4302
OY	4315	CTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAAATGCACTTTATACG	4374
Db	4303	CCAACCTAACAAACTCTGTTAATGTGTGACTTACCGTGGATACTAAATGGGTGTATTCAG	4362
OY	4375	AGCCTCGCCCATTTGGCAACCCGTTAATCTCACCCGCTCGTAAATGTGTATATCAAT	4434
Db	4363	AGCCTCGCCCATTTGGCAACAGATACTGCACTCTGTAATCTGTAAATCTCTGTTATCAAT	4422
OY	4435	AAACCGGTTAATGTGTACGTTGAACCTTGGTGTCAATGTCCTAATATCTTATCTGTGTC	4494
Db	4423	AAACCGTTAATGTGTTCAGTTTCACTGTGAATCTGTGTGCTCTGCGATATTTCTTCTTATCTAGTT	4482
OY	4495	ACCATAGCAACCGGTTACACATTAACTGTTAGTTGGCTTGGCA---ATVACCCCTAG	4550
Db	4483	TCCATGGCTAGTATGATTAAGATGAGTGGCGGTTAATCATTAATTAAGAAACCCCTAG	4542
OY	4551	TGAATGAGTGGCCCACTCCCTCTATATGGCGCTGCTGTGCGTGGGGCGGAGACAG	4610
Db	4543	TGAATGAGTGGCCCACTCCCTCTGTGGCGCTGCTGTGCTCACTGAAGCGGGGACACAA	4602
OY	4611	AGCTCTGCGCTCTCGGACCTTTTGTGTCCGAGGCGCCACCGAGGACGAGCGGCATAG	4670
Db	4603	AGCTGTGCGCCAGCGCCGGGCTTTCCCGGGGAGGCTCAGTAGAGGACGAGCGGCAGAG	4662
OY	4671	AGGAGTGTGCCAA4683	
Db	4663	AGGAGTGTGCCAA4675	

RESULT 14
US-09-770-315-3
; Sequence 3, Application US/09770315
; Patent No. 6429001
; GENERAL INFORMATION:

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; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Recombinant AAV Packaging Systems
; FILE REFERENCE: 20263-501
; CURRENT APPLICATION NUMBER: US/09/770,315
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,536
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7557
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant DNA
US-09-770-315-3

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Query Match	66.5%	Score 3114.4;	DB 3;	Length 7557;
Best Local Similarity	81.7%;	Pred. No. 0;		
Matches 3705; Conservative	0;	Mismatches 771;	Indels 58;	Gaps 7

OY	18	GGGCGCTGCTGAGCTACAGAGGCGGGGGGACCAAAAGTCCCGACGCGCCGGGCTTTGC	77
Db	4	GGCGCTGCTGCTCACTGAGGCGCCCGGGCAAAAGCCGGGCGTGGGGCGACTTTTGG	63
OY	78	CCGGGCGGCTCAGTGAAGGAGGACGCGCAGAGAGGAGTGGCCAACTCCATCACTAG	137
Db	64	TGCGCCGGCTCAGTGAAGGAGGACGCGCAGAGAGGAGTGGCCAACTCCATCACTGA	123
OY	138	GGG-----TTCTGAGGGGTGG	155
Db	124	TGGGACTTGACATTACTTGATATGATATGCTATACGAGTTATCCGGAGGGGTGG	183
OY	156	AGTCTGACGTGAATTAATACGTCAATAGGGTTAAGGAGGTCTGTATTTAGAGGTCACTGAGT	215
Db	184	AGTCTGACGTGAATTAATCCTCAATAGGGTTAAGGAGGTCTGTATTTAGAGGTCACTGAGT	243
OY	216	GTTTTCGACATTTTGGCGACACCATGTGTCAACGTGGGGATTTAAGCCCGAATGACAC	275
Db	244	GTTTTCGACATTTTGGCGACACCATGTGTCAACGTGGGGATTTAAGCCCGAATGACAC	303
OY	276	GCAGGGTCTCCATTTTGAAGCGGGAGTTTGAACGCGCAG-CGCGCATGCGGGGTTTAC	334
Db	304	GCAGGGTCTCCATTTTGAAGCGGGAGTTTGAACGCGCAGCGCCCATGCGGGGTTTAC	363
OY	335	GAGATTGTGATTAAGGTCCCGACGCACTTTGACGAGCATCTGCGCGCATTTCTGACAGC	394
Db	364	GAGATTGTGATTAAGGTCCCGACGCACTTTGACGAGCATCTGCGCGCATTTCTGACAGC	423
OY	395	TTTGTGAACGTGGGTGGCGGAAAGGAAATGGAGATTGCCCGCAATTTCTGACATGATCTG	454
Db	424	TTTGTGAACGTGGGTGGCGGAAAGGAAATGGAGATTGCCCGCAATTTCTGACATGATCTG	483
OY	455	AATCTGATTGAGCAGGCAACCCCTGACCGTGGGCGAGAACTGCGAGCGCATCTCTGTGC	514
Db	484	AATCTGATTGAGCAGGCAACCCCTGACCGTGGGCGAGAACTGCGAGCGCATCTCTGTGAG	543
OY	515	CATTCGCGCCCGGTGATTAAGGCCCGCGAGGCCCTCTCTTTGTTCAGTTTGAAGAGGC	574
Db	544	GAATTCGCGCCCGGTGATTAAGGCCCGCGAGGCCCTCTCTTTGTTGCAATTTGAAGAGGGA	603
OY	575	GAGTCTCACTTCCACTCCATATTCTGTGTGAGAACCAAGGGGGTCAAATTCATGTGTCTG	634
Db	604	GAGAGCTCACTTCCACTCCATGTGCTGTGTGAGAAACCAAGGGGGTGAATTCATGTGTGTG	663
OY	635	GGCGGCTTCTGAGTCAAGATTAGCGCAAGCTGTGCACACCATCAACGCGGGATTCGAG	694
Db	664	GGAGCTTCTGAGTCAAGATTGCGCAAAAATCTGATTCAGAGAAATTAACCGCGGGATTCGAG	723
OY	695	CCGACCTTCGCCCACTGGTTGCGGGTGACCAAGACGCGTAAATGCGCGAGGGGGGAAC	754
Db	724	CCGACTTTGGCAAACCTGGTTGCGGGTGACCAAGAAATGCGCGCGAGGGGGGAAC	783

QY	755	AAAGTGTGTGAACGAATGCTACATCCCAACTACCTTCGTGCCAGACATCAGCCGAGCTG	814
Db	784	AAAGTGTGTGAATGAATGCTACATCCCAACTACTTGTCTCCCAAAACCAGCTGTAGCTC	843
QY	815	CAGTGGGGGTGGAACCTAACATGAGAGAGATATATAAGCGGTGTATTAACCTGGCCGAGGCC	874
QY	875	AAACCGGCTGTGGCCGACGACCTGTGACCCACGTCAGCCAGACCAGAGACAAACAAGAG	934
Db	904	AAACGGTGTGTGGCCGACGACTGTGACGACGTCGTGCGAGACCGACAGAGACAAAGAAG	963
QY	935	AATCTGAACCCCAATTTCTGAGCGCGCTGTATCATCCGGTCAAAAACTCCGACGCTACATG	994
Db	964	AATCAGAAATCCCAATTTCTGATGCGCCGGTGTATCAGATCAAAAACTTCAGCCAGGTACATG	1023
QY	995	GAGCTGTGTGGGTGTGCTGTGTGACCCGGGGCATCATCTCCGAGAAACATGTGATCCAGAG	1055
Db	1024	GAGCTGTGTGGGTGTGCTGTGTGACAAAGGGGATTTACTGTGGAGAAACAATGTGATCCAGAG	1083
QY	1055	GACACGAGGCTGTGTATCTCTCTTCAACGCCCTCTCAACTGCGGGTCCAGATCAAGACC	1113
Db	1084	GACACGAGGCTGTATATCTCTCTTCAATGGGCTCTCAACTGCGGGTCCCAATCAAGGCT	1144
QY	1115	GCTCTGGAACAATGCCGGCAAGATCATGGCGGTGACCAAAATCCGCGCCGACTACTGTGTA	1174
Db	1144	GCTTTGACAAATGGCGGAAAGATTTATGAGCTGACTAAACCGGCCCGGACTACTGTGTG	1203
QY	1175	GCCCCCGCTCCGCCCGCCGACATTTAAACAAACGCAATTTACCGCATCTCTGAGCTGAAC	1233
Db	1204	GGCCACAGCCCGGTGGAGGACATTTCCACGACATCGGATTTATAAATTTGGAACTTAAC	1263
QY	1235	GAGTACGACCCGTGCTACGCGCGGCTCCGTCCTTCTCCGCTGGAGCCAGAAAAAGTTGGGA	1294
Db	1264	GAGTACGATCCCAATATGTCGGCTTCGTCCTTCTGGGATGGGCGCAGAAAAAGTTGGGC	1322
QY	1295	AAACGCAACAACATCTGGCTGTTTGGCGCGGCAACAAGGGCAAGACCAACATCGCGAA	1355
Db	1324	AAAGAGAACACATCTGGCTGTTTGGCGCTGCTGCACTACCGGGAAGACCAACATCGCGAG	1383
QY	1355	GCCATCGCCACGCGCGTCCCTTCTACGGCTGCGTCAACTGGAACCAATGAGAACTTTCCC	1411
Db	1384	GCCATAGCCCACTAGTGCCTCTTCTACGGGTGCGTAACTGGAACCAATGAGAACTTTCCC	1443
QY	1415	TTCAACGATTCGCTGCAACAATGTGTATCTGTGTGGAGGAGGCGCAATGACCGGCCAAG	1474
Db	1444	TTCAACGATTCGTGTGCAACAATGTGTATCTGTGTGGAGGAGGCGCAATGACCGGCCAAG	1503
QY	1475	GTCGTGAGTCCGACCAAGGCCATTTCTCGGCGGCAAGAGTGGCGGTGACCAAAAGTGC	1534
Db	1504	GTCGTGAGTCCGACCAAGGCCATTTCTCGGAGGAAAGCAAGTGGCGGTGACCAAAAGTGC	1563
QY	1535	AAGTGTCCGCCAGATCGATCCACCCCGGTGATCGTCACTTCAACACCAACATGTC	1594
Db	1564	AAGTCTCTCGGCCAGATGACCCGACTCCGTCATCCCTCAACACCAACATGTC	1623
QY	1595	GCCGTGATTTGACGGGAACAGCACCACTTCAAGCAACAGACGCGCTTGCAGAGACCGATG	1655
Db	1624	GCCGTGATTTGACGGGAACCTCAACGACCTTCAACACCAAGACGCGCTTGCAGAGACCGATG	1683
QY	1655	TTCAAAATTTGAACCTCACCCGCCGTCTGGAGCATGTTTGGCAAGTGAACAAACAGAGA	1714
Db	1684	TTCAAAATTTGAACCTCACCCGCCGTCTGGATATGACTTTTGGAAAGTCAACAAAGCAGAA	1743
QY	1715	GTCAAAGAGTTCTTCCGCTGGGCGCAGGATCAGCTGACCGAGTGTGGCATGAGTTCTAC	1774
Db	1744	GTCAAAGACTTTTCCGGTGGCAAAAGATCAGCTGTTGAGTGTGGACATGAAATTTCTAC	1803
QY	1775	GTCAGAAAGGTGTGAGCAACAACAAGCCGCCCATGACGCGGATTAACAGCAAGCAGCC	1834
Db	1804	GTCAGAAAGGTGTGAGCCAGAAAAAGACCGGCCCATGACGCGAGATATTAAGTGAACCC	1863
QY	1835	AAGCGGCGCTGCGCCCTCAGTCTCGCGGATTCATCTGACGTCAGACGCGGAAAGGACTCCGGTG	1894

Db 1864 AAACGGGTGCGGAGTCAAGTTGGCCGAGCCATGACGTGACAGCGCGA---AGCTTCGATC 1920
Qy 1895 GACTTGGCCGACAGGTACCAAAACAATGTTCTGTCACGGGGATGCTTCAATGCTG 1954
Db 1921 AACTACGAGACAGGTACCAAAACAATGTTCTGTCACGGGGATGCTTCAATGCTG 1980
Qy 1955 TTTCCCTGCAAAACAATGCGAGAGATGATCAATGATTTCAATTTGCTTCAGCAGCGG 2014
Db 1981 TTTCCCTGCAACATGCGAGAGATGATCAATGATTTCAATTTGCTTCACCTCAGCA 2040
Qy 2015 ACCAGAGCTGTTCAGAATGTTTTCCCGGCGTGTCAAGATCTCAACCGGT---CGTCA 2071
Db 2041 CAGAAAGACTGTTAGAGTGTCTTCC---CGTGTCAAGATCTCAACCGGTTCTGTGCTG 2097
Qy 2072 AAAGAGAGATTCGAAACTCTGTGCCATTCATCATCTGTGGGCGGGCTCCGAGATT 2131
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Db 2215 ATGATTTAATCAGGTATGCTGCGATGCTGATGTTATCTTCCAGATTGCTCGAGACAACCT 2274
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Db 2275 CTCTGAAGGAATTAAGACAGTGGTGAAGCTCAAACTGGCCCAACCAACCAAGCCCGC 2334
Qy 2312 CCAGCAAAAGCAGAGACGACGCGCGGGGTCTGGTCTTCTGATCTCAAGTACTCTGAGACC 2371
Db 2335 AGAGCGGCAATAAGACAGACAGAGGGGTCTTGTGTTCTTGGATCAAGTACTCTGAGACC 2394
Qy 2372 CTTCACCGGACTCGACAAAGGGGAGCCCGTCAACGCGCGAGATGACGCGCTTCGAGCA 2431
Db 2395 CTTCACCGGACTCGACAAAGGGGAGCCGCTCAACGAGGCAACGCGCGCGCTTCGAGCA 2454
Qy 2432 CGACAAAGGCTTACACACGACGAGCTCAAGCGGGTGAACATCCGTAACCTGCGGTATTAACA 2491
Db 2455 CGACAAAGGCTTACACACGAGCTCAAGCGGGTGAACATCCGTAACCTCAAGTATTAACA 2514
Qy 2492 CGCGGACGCGGAGTTTCAAGAGCGCTCTCAAGAAAGTACGTCTTTGGGGGCAACCTCGG 2551
Db 2515 CGCGGACGCGGAGTTTCAAGAGCGCTTAAAGAAATACGTCTTTGGGGGCAACCTCGG 2574
Qy 2552 GCGAGCACTCTTCAAGGCAAGAGGGTTCTCGAACCTTTGTGTTGAGGAAG 2611
Db 2575 ACGAGCACTCTTCAAGGCGAAGAGGGTTCTTGAACTCTGGGCGTGGTTGAGGAACC 2634
Qy 2612 TGCATAAGCGGCTCTGGAAGAAAGAAACGTCCGGTGAAGAGTCCGCAACAAGCCAGACTC 2671
Db 2635 TGTATAAGCGGCTCTGGGAAAAAAGAGGCGGTAGAGCACTCTCTGTGAGCCAGACTC 2694
Qy 2672 CTCCTCGGGCAATTGGCAAGACGAGCAGCAGCCGCTAAAAAGAGACTCAATTTTGCTCA 2731
Db 2695 CTCCTCGGGAAACGGAAAGCGGGCGAGCAGCAGCTGCAAGAAAAAGATTGAATTTTGCTCA 2754
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Db 2995 CCTCTACAAACAAATTTTCAGCCCAATCA---GGAGCTCGAAGCAATCACTACTTGG 3051
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Qy 3152 GCTCTCAACATCCAACTCAAGAGGCTCAAGAGGAATGAGGGGTCAAGCACTGTGTTAA 3211
Db 3172 GCTCTTAACTTCAAGTCAAAAGGCTCAGAGAAATGAAGTATCGACGAGATTGCTCA 3231
Qy 3212 TAACTTACAGACAGGTTCAAGTCTTGTGCGACTCGAGTACCAATTCCTGACGTCT 3271
Db 3232 TAACTTACAGACAGGTTCAAGTGTTTACTGACTGGAGTTACAGCTCCGTAACGTCT 3291
Qy 3272 CGGCTTGCAGACCAAGGCTGCTCTCCCTCGTTCCGGCGGAGGTGTTCAATTCGCA 3331
Db 3292 CGGCTCGGCGCATCAAGAGATGCTCCCGCGTTCCGACGAGAGTCTCATGTGTCACA 3351
Qy 3332 GTACGCTACCTTAACGCTCAACAATGGCAGCAGGCGAGTGGAGCGCTCATCTTTACTG 3391
Db 3352 GTATGATATCTTCAACCTGAAACAAGGAGTCAAGGAGTGAAGAGCTTCAATTTACTG 3411
Qy 3392 CTGGAATATTTCCATCGGAGATGTGAGAAAGGGCAATTAACCTTCACTCACTAC 3451
Db 3412 CTGGAATATTTCCATCGGAGATGTGAGAAAGGGCAATTAACCTTCACTCACTAC 3471
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Db 3472 TTTTGAAGAGTGTCTTCCACAGAGCTTACGGTCAAGCAGAGTCTGAGCGGTCTCAT 3531
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Qy 3992 TGTGCATGTTATGGAGCTTACCTGGAATGTGTGTGCAAGACAGACGATTAACCTGCA 4051
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Oy	4052	GGGTCCTATTTGGGCAAAATTCCTCACAAGGATGGAACCTTCAACCGCTCTCCCTCAT	41111
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Oy	4112	GGGGCGCTTTGGACTTAAGCACCCGCGCTCTCAGATTCCTCATCAAAAACAGCGCTGTCC	41717
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RESULT 15
US-09-438-268-5
Sequence 5, Application US/09438268
Patent No. 6491907
GENERAL INFORMATION:
APPLICANT: Rabinowitz, Joseph E.
APPLICANT: Samulek, Richard J
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: VIRUS VECTORS AND METHOD OF MAKING AND ADMINISTERING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 5470-186
CURRENT APPLICATION NUMBER: US/09/438,268
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,840
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/123,651
EARLIER FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 8179
TYPE: DNA
ORGANISM: Virus
US-09-438-268-5

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Query Match	64.2%	Score 3008;	DB 3;	Length 8179;
Best Local Similarity	82.2%;	Pred. No. 0;		
Matches 3547;	Conservative	0;	Mismatches 750;	Indels 19;
				Gaps 7;

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QY	251	TGGTATTATTAAAGCCGAGTGAAGCAGCAGAGTCTCATTTTGAAGCGGAGATTGACG <td>310</td>	310
Dp	181	TGGGTATTAAACCCGAGTGAAGCAGCAGAGTCTCATTTTGAAGGGGAGATTGACG <td>240</td>	240
QY	311	CGCAG- CGCCATGCGCGGGGTTTACGAGATGTGATTTAAGTCTCCACGACCTTGACGA <td>369</td>	369

Db	241	CGACACC	CGC	ATG	CCG	GGG	TTT	TAC	GAG	TAT	TGAT	TTA	AGT	TCC	AGG	ACT	TGA	CGG	300
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Db	301	GCATCTG	CCCG	GCAT	TTT	CTG	ACG	TTT	TGT	GAA	CTG	GGT	GGC	CGG	AGAG	AGAT	TGG	AGTT	360
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QY	550	CTTCTTT	GTG	CA	T	TG	CA	T	TG	CA	T	TG	CA	T	TG	CA	T	TG	609
Db	481	TTTCTTT	GTG	CA	T	TG	CA	T	TG	CA	T	TG	CA	T	TG	CA	T	TG	540
QY	610	CACGGGG	GGT	CA	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	669
Db	541	CACCGGG	GGT	CA	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	600
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Db	601	TCAGGAA	TTT	TAC	CGG	GGAT	CG	AT	CG	AC	CCG	CGC	CGA	CT	GGG	AT	CG	CA	660
QY	730	GCGTAT	TG	GGC	CCG	AGG	GGG	GA	CA	AGT	GGT	TGA	CG	AGT	CT	CA	T	CC	789
Db	661	CAGAA	ATG	GGC	CCG	AGG	GGG	GA	CA	AGT	GGT	TGA	CG	AGT	CT	CA	T	CC	720
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QY	1090	CAACTG	CG	GGT	CC	CG	AT	CA	AG	CG	CG	CT	CT	GG	CA	AT	GG	CG	1144
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Search completed: June 13, 2006, 13:19:47
Job time : 867 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 13:05:23 ; Search time 149 Seconds
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Title: US-10-696-261-19

Perfect score: 4683

Sequence: 1 ttggccactccctctctgcg.....cgcatagaggagtcgccaa 4683

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA New:*

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- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US00_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3244.2	69.3	4675	US-11-327-357-1	Sequence 1, Appli
2	125	2.7	145	US-11-327-357-2	Sequence 2, Appli
3	118.2	2.5	4675	US-11-327-357-1	Sequence 1, Appli
4	117.8	2.5	145	US-11-327-357-2	Sequence 1, Appli
5	110	2.3	8322	US-11-269-117-6	Sequence 2, Appli
6	110	2.3	8322	US-11-269-117-6	Sequence 6, Appli
7	52	1.1	1309	US-10-953-349-16574	Sequence 16574, A
8	47.2	1.0	1191	US-10-953-349-32993	Sequence 32993, A
9	47	1.0	1302	US-10-953-349-33793	Sequence 33793, A
10	46.6	1.0	845	US-10-953-349-27324	Sequence 27324, A
11	45	1.0	45	US-10-513-348-6	Sequence 6, Appli
12	43.6	0.9	2152	US-10-953-349-38921	Sequence 38921, A
13	43.4	0.9	1439	US-10-953-349-32310	Sequence 32310, A
14	43.2	0.9	48	US-10-953-349-32310	Sequence 32310, A
15	43.2	0.9	681	US-10-984-694-1	Sequence 1, Appli
16	43.2	0.9	3508	US-11-071-896-6	Sequence 2, Appli
17	42.6	0.9	926	US-10-953-349-38418	Sequence 38418, A
18	41.8	0.9	1291	US-10-953-349-34039	Sequence 34039, A
19	41.6	0.9	681	US-10-984-694-6	Sequence 6, Appli
20	41.6	0.9	1235	US-10-953-349-27792	Sequence 27792, A
21	41.6	0.9	1478	US-10-953-349-32700	Sequence 32700, A
22	41.6	0.9	3546	US-11-071-896-9	Sequence 9, Appli
23	41.6	0.9	3690	US-10-525-318-3	Sequence 3, Appli
24	41.6	0.9	5170	US-10-525-318-11	Sequence 11, Appli
25	41.6	0.9	5600	US-10-525-318-13	Sequence 13, Appli

26	41.6	0.9	6600	US-10-525-318-5	Sequence 5, Appli
27	41.6	0.9	7000	US-10-525-318-8	Sequence 8, Appli
28	41	0.9	1147	US-10-953-349-16567	Sequence 16567, A
c	29	0.9	1337	US-10-953-349-35245	Sequence 35245, A
30	41	0.9	1493	US-10-953-349-34059	Sequence 34059, A
31	41	0.9	1828	US-10-953-349-27343	Sequence 27343, A
32	40.8	0.9	1961	US-11-071-896-5	Sequence 5, Appli
33	40.8	0.9	3468	US-11-071-896-1	Sequence 1, Appli
34	40.8	0.9	3546	US-11-071-896-3	Sequence 7, Appli
35	40.8	0.9	3546	US-11-071-896-7	Sequence 11, Appli
36	40.8	0.9	3547	US-11-071-896-11	Sequence 11, Appli
37	40.6	0.9	1667	US-10-953-349-31278	Sequence 31278, A
38	40.4	0.9	696	US-10-953-349-16066	Sequence 16066, A
c	39	0.9	1570	US-10-953-349-27031	Sequence 27031, A
40	40.2	0.9	684	US-10-953-349-39243	Sequence 39243, A
41	40.2	0.9	717	US-11-252-276-45	Sequence 45, Appli
42	40.2	0.9	717	US-11-252-276-47	Sequence 47, Appli
43	40.2	0.9	717	US-11-252-276-49	Sequence 49, Appli
44	40.2	0.9	1498	US-10-953-349-31731	Sequence 31731, A
45	40.2	0.9	1623	US-11-252-276-33	Sequence 33, Appli

ALIGNMENTS

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RESULT 1
US-11-327-357-1
; Sequence 1, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
; APPLICANT: BPG International Ltd
; APPLICANT: BEARD DR, PETER
; APPLICANT: RAU DR, KENNETH
; TITLE OF INVENTION: CYTOTOXIC AGENTS
; FILE REFERENCE: 14218440
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/327,357
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4675
; TYPE: DNA
; ORGANISM: adeno-associated virus 2
US-11-327-357-1

Query Match      69.3%; Score 3244.2; DB 7; Length 4675;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

QY      1 TTGGCACTCCCTCTGCGGCTGCTGCTGCTCACTAGAGCGCGGCAACAAAGTGGCC 60
DB      1 TTGGCACTCCCTCTGCGGCTGCTGCTGCTGCTCACTAGAGCGCGGCAACAAAGTGGCC 60

QY      61 CGAGCCCGGGCTTTGCCCGGGCGGCTCACTAGAGCGAGCGCGCAAGAGGAGTG 120
DB      61 CGAGCCCGGGCTTTGCCCGGGCGGCTCACTAGAGCGAGCGCGCAAGAGGAGTG 120

QY      121 GCGAATCATCACTATAGGGGTTCTGAGGGGTGAGTCCGTGACGTAATTAAGTCTAG 180
DB      121 GCGAATCATCACTATAGGGGTTCTGAGGGGTGAGTCCGTGACGTAATTAAGTCTAG 180

QY      181 GGTAGGAGGTCCTGTATTAGAGTCACTGAGTGTTTTGCACATTTTGCACACAT 240
DB      181 GGTAGGAGGTCCTGTATTAGAGTCACTGAGTGTTTTGCACATTTTGCACACAT 240

QY      241 GTGTACGCTGGGTATTAAAGCCGAGTGAAGCAAGAGGTCCTCAATTTTGAAGCGGA 300
DB      241 GTGTACGCTGGGTATTAAAGCCGAGTGAAGCAAGAGGTCCTCAATTTTGAAGCGGA 300

QY      301 GGTGAAGCGGAG-CGCCATGCCGGGGTTTACGATTTGATTAAAGTCCCGAGCG 359
DB      301 GGTGAAGCGGAG-CGCCATGCCGGGGTTTACGATTTGATTAAAGTCCCGAGCG 359
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Dh 301 GATTGAACGGCCAGCCCATATGCGGGTTTATCGAATTGTGATTAAGTCCCCAGCG 360
Qy 360 ACCTTGACGACATCTGCCCGGCAATTTGTGACAGTTTGTGAACCTGGGTGGCCGAGAGG 419
Dh 361 ACCTTGACGGGCATCTGCCCGGCAATTTGTGACAGTTTGTGAACCTGGGTGGCCGAGAGG 420
Qy 420 AATGGAGTTTCCCGCAGATTTCTGCATGATCTGAACTGTAATTGAGGAGCACCCTGTA 479
Dh 421 AATGGAGTTTCCCGCAGATTTCTGCATGATCTGAACTGTAATTGAGGAGCACCCTGTA 480
Qy 480 CCGTGGCCGAGAGTGTGACGGCGCATCTTCTGTGTCACATGCGCGCGGTGAGTAAGGCC 539
Dh 481 CCGTGGCCGAGAGTGTGACGGCGCATCTTCTGTGTCACGGAATGGCCGCGTGTGATTAAGGCC 540
Qy 540 CGGAGGCCCTCTTCTGTGTTGATTCGAGAGGGGCGAATCTTACTTCCACCTCCATATTC 599
Dh 541 CGGAGGCCCTCTTCTGTGTTGATTCGAGAGGGGCGAATCTTACTTCCACATGCAATGCG 600
Qy 600 TGTGAGAACCAAGGGGCTCAATCTCATGTGTGCTGGCCGCTTCTGATGATGATAGCG 659
Dh 601 TGTGAGAACCAAGGGGCTCAATCTCATGTGTGCTGGCCGCTTCTGATGATGATAGCG 660
Qy 660 ACAAGCTGTGTGACACCACTTACCGCGGATGAGCCGACCTTGCCCACTGTGTTCCGGG 719
Dh 661 AAAAACTGATTCAGGAATTTACCGCGGATGAGCCGACTTTGTCMAACTGTGTTCCGGG 720
Qy 720 TGACCAAGACCGGTAAATGCGCGGAGGGGGAACAAGTGTGTGAGAGATGATATCC 779
Dh 721 TCACAAACACCAAAATGCGCGGAGGGGGAACAAGTGTGTGAGAGATGATATCC 780
Qy 780 CCAACTACCTCTGCGCCCAAGACTGACCGCGAGCTGCAATGAGCGGTGATTAACATGAGG 839
Dh 781 CCAATTAATCTTCTGCGCCCAAGACTGACCGCGAGCTGCAATGAGCGGTGATTAATGAGG 840
Qy 840 AGTATATAAGCGCGCTGTTAAACTGTGGCGAGCCGCAACCGCTGTGGCGACGACTGTA 899
Dh 841 AGTATATAAGCGCGCTGTTAAACTGTGGCGAGCGTAAACGGTGTGGCGAGACTGTA 900
Qy 900 CCGCAGTCAGCCAGCCAGAGGAGCAAGAGAACTGAACTCCCAATCTGACCGCGC 959
Dh 901 CCGCAGTCAGCCAGCCAGAGGAGCAAGAGAACTGAACTCCCAATCTGATGCGC 960
Qy 960 CTGTGATCCGGTCAAAAACTTCGCGACGCTACATGAGACTGTGCGGTGCTGTGAGCC 1019
Dh 961 CCGTGTATCAGATCAAAAACTTCAGCGAGCTACATGAGACTGTGCGGTGCTGTGAGCA 1020
Qy 1020 GGGGCTATCACTCCGAGAGAGAGTGTATCCAGAGGACCAAGCCCTGTAATCTTCTTCA 1079
Dh 1021 AGGGGATTTACTTCGAGAGAGAGTGTATCCAGAGGACCAAGCCCTGTAATCTTCTTCA 1080
Qy 1080 ACGCGGCTCCCAACTCGCGGTCGCCAGATCAAGGCGGCTCTGGAACAATGCCGCAAGATCA 1139
Dh 1081 ATGCGGCTCCCAACTCGCGGTCGCCAGATCAAGGCTGCTTGTGACATGCGGAAAGATTA 1140
Qy 1140 TGGCGCTGACCAAACTCGCGGCCGACTTACTGTAGAGCCCGCTCGGCCCGCAATTA 1199
Dh 1141 TGAAGCTGACTTAAACCGCCCCGACTACTGTGTGGCCAGAGGCCGTGAGAGCAATTT 1200
Qy 1200 AAACCAACCGCATTTTACCGCATCTCTGAGCTGAACGGCTTAGACCTTGCTTACCGCGCT 1259
Dh 1201 CCACCAATCGGATTTTATTAATTTTGTGAATTAACGGGTAGATCCCAATATCGGGCTT 1260
Qy 1260 CCGTCTTCTCTGCGCTGGGCCCAAGAAAGTTTCGAAAGCAACCAATCTGGGCTTTT 1319
Dh 1261 CCGTCTTCTCTGCGCTGGGCCCAAGAAAGTTTCGAAAGCAACCAATCTGGGCTTTT 1320
Qy 1320 GGGCGGCAACCAAGGCAAGACCAACATCGCGAAGCATCGCCACGCGCTGCTTCT 1379
Dh 1321 GGGCGGCAACCAAGGCAAGACCAACATCGCGAAGCATAGCCCAACTGTGCTTCT 1380
Qy 1380 ACGGCTGTGTACACTGAGCAATGAGAACTTTCTTCAAGATTTGCGTGCACAAAGATG 1439
Dh 1381 ACGGCTGTGTAACTGAGCAATGAGAACTTTCTTCAAGATTTGCGTGCACAAAGATG 1440

Qy 1440 TGATCTGTGGAGAGGAGGCAAGATGACGGCCAAAGGTGTGAGTGTCCGCCAAGGCCATTC 1499
Dh 1441 TGATCTGTGGAGAGGAGGCAAGATGACGGCCAAAGGTGTGAGTGTCCGCCAAGGCCATTC 1500
Qy 1500 TCGCGGCAACCAAGGTGCGGTGGAACCAAAAGTGCAGGTGTGCGCCAGATCGATCCA 1559
Dh 1501 TCGGAGGAACCAAGGTGCGGTGGAACCAAAAGTGCAGGTGTGCGCCAGATCGATCCA 1560
Qy 1560 CCCCCTGTATCTGTACCTTCCCAACCAACTGTGCGCGGTGATTTGACGGGAACGACCA 1619
Dh 1561 CTCCCGTGTATCTGTACCTTCCCAACCAACTGTGCGCGGTGATTTGACGGGAACGACCA 1620
Qy 1620 CTTTGCAGACACGACGACCGTTGAGGACCGGATGTTCAAAATTTGAATCAACCGCGCTC 1679
Dh 1621 CTTTGCAGACACGACGACCGTTGAGGACCGGATGTTCAAAATTTGAATCAACCGCGCTC 1680
Qy 1680 TGAAGCATGACTTTGGCAAGGTGACAAAGCAGAAATCAAAAGATTTCTCGCTGGGCGC 1739
Dh 1681 TGAATCATGACTTTGGGAGGTGACCAAGCAGAAAGTCAAAAGATTTCTCGGTTGGGCAA 1740
Qy 1740 AGGATCAAGTGAACCGAGTGGCCGATGAGTTTCAAGTCAAGGATGAGGAGGCAACACA 1799
Dh 1741 AGGATCAAGTGTGAGTGGAGGATGATTAATCTTACGTCMAAAAGGTGAGCAAGAAA 1800
Qy 1800 GACCCGCCCCGATGACGCGGATTAAGCGAGCCAAAGCGGCGCTGCCCCAGTCCGCG 1859
Dh 1801 GACCCGCCCCGATGACGAGGATTAAGTGAACCCAAAGCGGCTGCGGATCGATTTGCGC 1860
Qy 1860 ATTCATGACGTGACGCGGAGAGAGCTCGGTGACTTTGCGGACAGGTACCAAAACA 1919
Dh 1861 AGCCATGACGTGACGAGCGGAG---AGCTTCGATCAACTACGACGACAGGTACCAAAACA 1917
Qy 1920 AATGTTCTGTCACGCGGAGATGCTTCAAGTGTGCTTCCCTGCAAAACATGAGAGAA 1979
Dh 1918 AATGTTCTGTCACGCGGAGATGATTAATGATGCTGTTCCCTGCAAGATGAGAGAA 1977
Qy 1980 TGAATCAGAAATTTCAACTTTGCTTCAACGACGCGGACAGAGACTGTCAGAAATGTTTC 2039
Dh 1978 TGAATCAGAAATTTCAAAATTTGCTTCACTCAACGAGCAAGAAAGCTGTTTGAATGCTTTC 2037
Qy 2040 CCGCGGTGTGAGAACTTCAACCGGT---CGTCAAAAAGAGAGCTATCGGAAACTCTGTG 2096
Dh 2038 C---CGTGTGAGAACTTCAACCGGTCTGCTGCTCAAAAAGGCTATCAAGAACTGTGCT 2094
Qy 2097 CCAATTCATCTGCTGCGGCGGCTCCGAGATGCTTCTGCGCTGCGATCTGGTCA 2156
Dh 2095 ACATTCATCATCATGAGGAAAGGTGACAG---CGTTGCACTGCTGCGATCTGGTCA 2151
Qy 2157 ACGTGTATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAACCAAGTATGCTGCC 2216
Dh 2152 ATGTGATTTGGATGACTGATCTTTGAAACAATTAATTAATTAAGTATGCTGCC 2211
Qy 2217 GATGTTATCTTCCAGTTGCTGTGAGGACCACTCTCTGAGGCAATTCGCGAGTGTG 2276
Dh 2212 GATGTTATCTTCCAGTTGCTGTGAGGACCACTCTCTGAGGAAATTAAGAGTGTG 2271
Qy 2277 GACTTGAACCTGGAAGCCCGGAAACCAAGCCAAACGAGAAAGAGAGAGCGAGCGG 2336
Dh 2272 AAGCTCAAACTGAGCCCAACCAACCAAGCCCGAGAGGAGATTAAGAGAGAGAGG 2331
Qy 2337 GGTCTGTGCTTCTGCTGCTCAAGTACTTGTGACCTTCAACGAGCTGCAAGAGGAGAG 2396
Dh 2332 GGTCTGTGCTTCTGCTGCTCAAGTACTTGTGACCTTCAACGAGCTGCAAGAGGAGAG 2391
Qy 2397 CCGTCAAGCGCGGAGTGAAGCGGCTTGTGACAGG-ACAAGGCTTACGACGAGCT 2455
Dh 2392 CCGGTCAAGCGGAGAGCGCGGCTTGTGACAGGCTTCAAGAGCTTACGACGAGCT 2451
Qy 2456 CAAAGCGGTGACCAATCTGCGGTATTAACCAAGCGGAGCGGAGTTTCAAGAGCG 2515
Dh 2452 GACAGGAGAGCAACCGTATCTCAAGTACCAACGCGGAGCGGAGTTTCAAGAGCG 2511

OY	2516	TCGCAAGAAGTACGTCTTTTGGGGGCACTCGGGGAGCAGTCTTCCAGGCCAAGA	2515
Db	2512	CCTTAAAGAAAGTACGTCTTTTGGGGGCACTCGGAGAGCAGTCTTCCAGGCCAAGA	2511
OY	2516	GAGGGTTCTCGAACCCTTTTGGCTGGTGAAGGAAGTCTAAGACGGCTCCGGAAAGA	2635
Db	2512	GAGGGTTCTTGAACCTCTGGGCTTGTAAGAACCTGTTAAGACGGCTCCGGGAAAAA	2631
OY	2636	AAGTCCGTAGAGCAGTGCACAAGACCGACCTCTCGGGCATTTGGCAAGACAG	2695
Db	2632	GAGGCCGGTTAAGCACTCTCGTGGACCGACAGCTCTCTCGGGAAACCGAAAGCCGG	2691
OY	2686	CCAGCAGCCCCCGTAAAAAGACCTCAATTTTGTGTCACTGGCGACTCAGAGTCATGCC	2755
Db	2692	CCAGCAGCCTTCAGAAAAAGATTGAATTTGTGTGAGCTGGAGACGCAAGCTCAGTAC	2751
OY	2756	CGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCGGCTGTGGGACCTACATCAAT	2815
Db	2752	TGAATCCCAAGCTCTCGGACAGCCACCGACGCCCTCTGTGTCTGGGAACTAATACAT	2811
OY	2816	GAGCTTCAGCGCGGTGGCGCAACAATGGCAGACATACAGAAAGCGCCGACGGAGTGGTTA	2875
Db	2812	GGCTACAGGCAAGTGGCGCAACAGTGGCAAGCATACGAGGGCCGACGGAGTGGTTA	2871
OY	2876	TGCCTCAGGAAATTGGCAATTTGGATTCACATGCTGGGCGACAGAGTCATCACCAAC	2935
Db	2872	TTCTCTCCGGAATTGGCAATTTGGATTCACATGATGGGCGACAGAGTCATCACCAAC	2931
OY	2936	CACCCGAACATGGGCTTGGCCCACTTAAACAACCACTCTACAGAGAAATCTCAGATGC	2995
Db	2932	CACCCGAACCTGGGCTTGGCCCACTTAAACAACCACTCTACAGAGAAATTTCCAGCA	2991
OY	2996	TTCAACGGGGGCGCAGCAAGCAACACACTACTTGGCTACACAGCAACCCCTGGGGATTT	3055
Db	2992	ATCA---GGAGCTTCGAACGACAACTACTTGGCTACAGCAACCCCTGGGGATTT	3048
OY	3056	TGATTTCAACAGATTCACATGCCATTTTCTACACAGTACGTGGCAGCGACTCATCAACA	3115
Db	3049	TGACTTCAACAGATTCACATGCCATTTTCTACACAGTACGTGGCAGCAAGACTCATCAACA	3108
OY	3116	CAATTTGGGGAATTCGGGCCCAAGAGCTCACTTCAAGCTCTTCAACATCCAAATCAAGA	3175
Db	3109	CAACTGGGGAATTCGAGCCCAAGAGCTCAACTTCAAGCTCTTCAACATTCAAAGTCAAGA	3168
OY	3176	GATCAAGACGAATGATGGCGTCAAGACCATGCGCTAACTTACCTTACAGACAGTTCAGT	3235
Db	3169	GGTCAAGCAAGATGACGATGACGACGACATTTGCCAATACCTTACAGACAGTTCAGT	3228
OY	3236	CTTGTCCGACTCGAGATCAAGATTCGCTCCGTAAGTCTCTCGGCTCTGGCACCAGGCTGCT	3295
Db	3229	GTTTACTGACTCGAGATCAAGATTCGCTCCGTAAGTCTCTCGGCTCTGGGACTCAAGGATGCT	3288
OY	3286	CCCTTCGTTCCCGGGGAGCGTGTCTATGATTTCCGAGATACGGCTACCTAACGCTCAACA	3355
Db	3289	CCCGCGGTTCCAGAGAGCGTCTCTATGTGTGCACAGATAGGAATACCTCACCTCGAACAA	3348
OY	3356	TGGCAGCCAGGAGATGGGACGCTCATCTTTTACGCTGGAAATTTCCCATGCGCAGAT	3415
Db	3349	CGGAGATGAGGCAATGAGACGCTCTTCAATTTTACGCTGGAGATTTCTTCTTCAGAT	3408
OY	3416	GCTGAGAACGGGCAATTAATTTTACCTTCAGCTACACTTTCAGAGACGTCCTTTCACAG	3475
Db	3409	GCTGGGTACCGGAAACAATTTTACCTTCAGCTACACTTTCAGAGACGTCCTTTCACAG	3468
OY	3476	CAGCTACCGGCACAGCCAGACGCTGGACCGGCTATGAATCTCTCATACACAGTACT	3535
Db	3469	CAGCTACCGCTACAGCCAGAGCTGGACCGTCTCATGTATCTCTCATACAGCAGTACT	3528
OY	3536	GTATTACCTGAACAGAACTCACAATCACTCAGTCCGGAAGTCCCAAAACAAGACTTGCCTT	3595
Db	3529	GTATTACTTGAAGCAAAACATCTCAAGTGAACCAACGCAAGTAAAGCTTCACTT	3588
OY	3596	TAGCCGTGGGTCTCAGCTGGCAATGTCTTTCAGCCCAAAACATGGACTCTGGAACCTG	3655

Db	3589	TTCTAGGCGCGAGAGTGA	CATTCCGGACAGCTAGGAAC	TGGCTTCTCGAACCTTG	3648	
Oy	3656	TTACCGGAGAGCGCGT	TTTAAAAA	CAAAAACAGACAACA	CAGCACTTACCTG	3715
Db	3649	TTACCGCAGACGAGAT	ATCAAAAGACATCTGCGGAT	TAACAACAACA	CAGTGAATCTCGTG	3708
Oy	3716	GACTGGTCTTCAAAAT	ATAACTTAACTTAATGGCGTGAAT	CTATTAATCAACCTG	GCACTGC	3775
Db	3709	GACTGAGCTACCAAG	TACCACTTCAATGGCAGAGACTCTCGGTGAATC	-----CGGC	3762	
Oy	3776	TATGGCTCAACAAG	ACGAACAAATTTCTTCCATGACGGGTG	CATGATTTT	3835	
Db	3763	CATGCAACCAAGCA	GAGCGATGAAGAAATTTTTTCTCAGAGCGGGT	TTCTCATTT	3822	
Oy	3836	TGAAAGAGAGCGCGG	AGCTTAAACACTGCATTTGACAATG	ATCATGACAGCA	3895	
Db	3823	TGGAGACGACGCTC	AGAGAAA	CAATGTGAACATTGAAAAGT	CATGATTAACAGCA	3882
Oy	3896	AGAGAAATCAAAGC	ACTTAAACCCGTGGCCACGGAAGATTTG	GGACTGAGCTCA	3955	
Db	3883	AGAGAAATCGGAAT	CAACCAATCCCGTGGTACGGAGCAGTATG	TTCTGATCTACCA	3942	
Oy	3956	TCTCCAGACGACGAC	ACAGACCTGCGACCGGAGATGTGCATGT	ATGGAAGCTTACC	4015	
Db	3943	CCTCCAGAGAGCA	CAGAGAGCAGCTACCGCAGATGTCA	CAACAGGCGTTCTTCC	4002	
Oy	4016	TGGAATGGTGTGGCA	AGACAGAGATTA	CTGAGAGGCTCTATTG	GGGCAAAATTC	4075
Db	4003	AGCGATGTTGGGAC	GACAGAGATGTACTTCAAGGCGCCATCT	GGCAAAAGATTC	4062	
Oy	4076	TCACAGGATGGA	CACTTCAACCGCTCTCTCATGGCGGCTT	TGCACTTAAGCACCC	4135	
Db	4063	ACACGAGCGGAC	ATTTCACCCCTCTCCCTCATGGTGGA	TTCCGACTTAAACACC	4122	
Oy	4136	GCTTCTCAGATCT	CATCAAAAACGCGCTGTTCTTGC	GAATCTCTCGGACGATTTTC	4195	
Db	4123	TCTCTCAGATCT	CATCAAGAACACCCCGGTAC	CTGCGAATCTTCGACCACTTCAG	4182	
Oy	4196	GGCTACAAAGTTG	TCATTCATCAACCCAGTATTTCC	ACAGAGACA-AGTAGCGTGAGACA	4254	
Db	4183	TGCGCAAAAGTTG	CTTCTTCTTCAACAATCTCCAGGACACG	GTACAGCTTGAGACA	4242	
Oy	4255	TTGAATGGAGCTG	AGAAAAGCAACGCTGGAATCCGAA	TGCACTATACAT	4314	
Db	4243	TGAGATGGAGCTG	AGAAAAGCAACGCTGGAATCCGAA	TTCAGTACACTT	4302	
Oy	4315	CTAACTATGCAAA	ATCTGCCAAGCTGATTTCACTGTGGACA	CAATGGAATTA	ACTG	4374
Db	4303	CCAACTACAA	CAATCTGTAAATGCTGACTTACCGTGA	ATACPAATGCGCTGATTCAG	4362	
Oy	4375	AGCTCGCGCCAT	TGGCAACCGGTAACTCACCGCCCTCGTAA	TGTGTATACAT	4434	
Db	4363	AGCTCGCGCCAT	TGGCAACGATACCTGACTCTGTAATGT	TTGTTTAACAT	4422	
Oy	4435	AAACCGGTTAAT	TGTGTCACTTGAATGTCTCATATTA	CTTAATCTGATC	4494	
Db	4423	AAACCGTTAAT	TGTGTCACTTGAATGTCTGTGCAATTTCTT	CTTAATCTGAT	4482	
Oy	4495	ACCATAGCA	CCGGTTACACTTAACTGTGAGCTTGGCA	---ATACCCCTAG	4550	
Db	4483	TCCATGGCTA	GTAGATTAATGATAGATGGCGGTTAATCAT	TAACTAACAGAACCCCTAG	4542	
Oy	4551	TGATGGAAT	TGCCACCTCCCTTAAATGGCGCTGCTGCTG	CTGAGGGGCGGACAGAGAG	4610	
Db	4543	TGATGGAAT	TGGCACTCTCTCTGGCGCTGCTGCTGCT	ACTAGAGCGGCGACCA	4602	
Oy	4611	AGCTCTGCGCT	CTGCGACCTTTTGATCGACAGGCCCA	CCGAGCGAGCGGCGCATAG	4670	
Db	4603	AGGTCGCCCA	CGCCCGGCTTTTCCCGGGGCGCTCAGTGA	GAGCGGCGGAGAG	4662	
Oy	4671	AGGAGTGGCAA	4683			

Db 4663 AGGAGTGGCCAA 4675

RESULT 2

US-11-327-357-2
; Sequence 2, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
; APPLICANT: BTG International Ltd
; APPLICANT: BEARD DR, PETER
; APPLICANT: RAJ DR, KENNETH
; TITLE OF INVENTION: CYTOTOXIC AGENTS
; FILE REFERENCE: 142184WO
; CURRENT APPLICATION NUMBER: US/11/327,357
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: 0009887.1
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: adeno-associated virus 2
; FEATURE:
; NAME/KEY: misc_structure
; LOCATION: (1)..(145)
; OTHER INFORMATION: ITR
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)
; OTHER INFORMATION: Unpaired base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (94)
; OTHER INFORMATION: Unpaired base
; US-11-327-357-2

Query Match 2.7%; Score 125; DB 7; Length 145;

Best Local Similarity 100.0%; Pred. No. 2,7e-24; Mismatches 0; Indels 0; Gaps 0;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 60
Db 21 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 80
Qy 61 CGAGCGCCGGGCTTTGGCCGGGCGGCTCACTGAGGCGGCGCAAGAGGAGTGG 120
Db 81 CGAGCGCCGGGCTTTGGCCGGGCGGCTCACTGAGGCGGCGCAAGAGGAGTGG 140
Qy 121 GCCAA 125
Db 141 GCCAA 145

RESULT 3

US-11-327-357-1/c
; Sequence 1, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
; APPLICANT: BTG International Ltd
; APPLICANT: BEARD DR, PETER
; APPLICANT: RAJ DR, KENNETH
; TITLE OF INVENTION: CYTOTOXIC AGENTS
; FILE REFERENCE: 142184WO
; CURRENT APPLICATION NUMBER: US/11/327,357
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: 0009887.1
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4675
; TYPE: DNA

; ORGANISM: adeno-associated virus 2
US-11-327-357-1

Query Match 2.5%; Score 118.2; DB 7; Length 4675;

Best Local Similarity 87.8%; Pred. No. 1e-21; Mismatches 18; Indels 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 60
Db 4675 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 4616
Qy 61 CGAGCGCCGGGCTTTGGCCGGGCGGCTCACTGAGGCGGCGCAAGAGGAGTGG 120
Db 4615 CGTCGGGCGACCTTTGGTTCGCCGCGCTCACTGAGGCGGCGCAAGAGGAGTGG 4556
Qy 121 GCCAACTCCACTAGAGGTTCTCG 147
Db 4555 GCCAACTCCACTAGAGGTTCTCG 4529

RESULT 4

US-11-327-357-2/c
; Sequence 2, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
; APPLICANT: BTG International Ltd
; APPLICANT: BEARD DR, PETER
; APPLICANT: RAJ DR, KENNETH
; TITLE OF INVENTION: CYTOTOXIC AGENTS
; FILE REFERENCE: 142184WO
; CURRENT APPLICATION NUMBER: US/11/327,357
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: 0009887.1
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: adeno-associated virus 2
; FEATURE:
; NAME/KEY: misc_structure
; LOCATION: (1)..(145)
; OTHER INFORMATION: ITR
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)
; OTHER INFORMATION: Unpaired base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (94)
; OTHER INFORMATION: Unpaired base
; US-11-327-357-2

Query Match 2.5%; Score 117.8; DB 7; Length 145;

Best Local Similarity 88.3%; Pred. No. 2,2e-22; Mismatches 17; Indels 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 60
Db 145 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGGGCGCAAGAGTGGCC 86
Qy 61 CGAGCGCCGGGCTTTGGCCGGGCGGCTCACTGAGGCGGCGCAAGAGGAGTGG 120
Db 85 CGTCGGGCGACCTTTGGTTCGCCGCGCTCACTGAGGCGGCGCAAGAGGAGTGG 26
Qy 121 GCCAACTCCACTAGAGGTTCTCT 145
Db 25 GCCAACTCCACTAGAGGTTCTCT 1

RESULT 5

US-11-269-117-6

```
/ Sequence 6, Application US/11269117
/ Publication No. US20060110364A1
/ GENERAL INFORMATION:
/ APPLICANT: LIN, et al.
/ TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
/ TITLE OF INVENTION: RECEPTORS
/ FILE REFERENCE: 28967/40835B
/ CURRENT APPLICATION NUMBER: US/11/269,117
/ CURRENT FILING DATE: 2005-11-08
/ PRIOR APPLICATION NUMBER: US 11/208,696
/ PRIOR FILING DATE: 2005-08-22
/ PRIOR APPLICATION NUMBER: US 60/602,926
/ PRIOR FILING DATE: 2004-08-20
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 6
/ LENGTH: 8322
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: AAV vector
US-11-269-117-6
```

```
Query Match          2.3%; Score 110; DB 7; Length 8322;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGCACTCCCTCTCTCTGCGCGCTCGCTCTCACTGAGCGCGGCGACCAAGGTCCG 60
DB      4625 TTGGCACTCCCTCTCTCTGCGCGCTCGCTCTCACTGAGCGCGGCGACCAAGGTCCG 4684
QY      61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGCGAG 110
DB      4685 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGCGAG 4734
```

```
RESULT 6
US-11-269-117-6/c
/ Sequence 6, Application US/11269117
/ Publication No. US20060110364A1
/ GENERAL INFORMATION:
/ APPLICANT: LIN, et al.
/ TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
/ TITLE OF INVENTION: RECEPTORS
/ FILE REFERENCE: 28967/40835B
/ CURRENT APPLICATION NUMBER: US/11/269,117
/ CURRENT FILING DATE: 2005-11-08
/ PRIOR APPLICATION NUMBER: US 11/208,696
/ PRIOR FILING DATE: 2005-08-22
/ PRIOR APPLICATION NUMBER: US 60/602,926
/ PRIOR FILING DATE: 2004-08-20
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 6
/ LENGTH: 8322
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: AAV vector
US-11-269-117-6
```

```
Query Match          2.3%; Score 110; DB 7; Length 8322;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGCACTCCCTCTCTCTGCGCGCTCGCTCTCACTGAGCGCGGCGACCAAGGTCCG 60
DB      116 TTGGCACTCCCTCTCTCTGCGCGCTCGCTCTCACTGAGCGCGGCGACCAAGGTCCG 57
QY      61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGCGAG 110
DB      56 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGCGAG 7
```

```
RESULT 7
US-10-953-349-16574
/ Sequence 16574, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ TITLE OF INVENTION: ENCODED THERAPY
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16574
/ LENGTH: 1309
/ TYPE: DNA
/ ORGANISM: Glycine max
US-10-953-349-16574
```

```
Query Match          1.1%; Score 52; DB 6; Length 1309;
Best Local Similarity 46.1%; Pred. No. 0.00022;
Matches 175; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
```

```
QY      1011 TGTGTGACCGGGGATCACTCCGGAAGACATGATCCAGAGACGAGGCTTGATCA 1070
DB      638 TGTGAGAGCTGTGTCTCTCTCTGCGCGGCGCACTCCATGGCGGTGCGGCTCTCTCT 697
QY      1071 TCTCTTCAACGCGGCTTCACTTCGCGTCCAGATCAAGCGCGCTTGACAAATGCCG 1130
DB      698 TCACCGGCGGCTCAACCGCGCGCGGAGGAGATCAACCGGCTTACCGCAACTTTC 757
QY      1131 GCAAGATATAGCGCTGACCAATTCGCGCGGCTGACTAGTACGCTCCGCGCG 1190
DB      758 ACCACAAAGTGCACCAAGGCGCCCAACCGCGCTGTGTCAACACTTCGCGATGAGACT 817
QY      1191 CCGACATTAAACCAACCGCATTTACCGCATCTGAGACTGAACGCTACGACCTTGCT 1250
DB      818 ACGAGACGCTGTCCAAATGTTATGCCGGGTTTACAGCGGCGGTGCGCAAGATCAGGACT 877
QY      1251 ACGCGGCTCGGTCTTTCTGCGGTGGGCGCAAAAAGTTTGGAAAACGCAACCATCT 1310
DB      878 TCTCTGACAAACCTTCTACCAACAACTTCGCGAGATGTCAGCTTCAACTCCGACT 937
QY      1311 GGCTTTTGGGCGGCGGCAACGCGGCAAGACCAATCGCGGAGCATTCGCCAGCGCG 1370
DB      938 GGCAGCTCATGACCCACCGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 997
QY      1371 TGCCCTTCTACGCGCTGCGTC 1390
DB      998 CGCTCTGGGACGCGGACTTC 1017
```

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RESULT 8
US-10-953-349-33293
/ Sequence 33293, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ TITLE OF INVENTION: ENCODED THERAPY
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 33293
/ LENGTH: 1191
/ TYPE: DNA
/ ORGANISM: Zea mays subsp. mays
```

```
US-10-953-349-33293
Query Match          1.0%; Score 47.2; DB 6; Length 1191;
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Best Local Similarity 44.3%; Pred. No. 0.0039;
Matches 193; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 1009 GCTGTGACCGGGGATCCTCCGAGAACGATGATCCAGAGAGACGAGCTCTGTA 1068
DB 473 GCTGCGGGGAAACAACCTGAGATGATCCCGCGGGGGCGGCGGAGCGGGTCTC 532
QY 1069 CATCTCTTCAACGCGGCTCCAACTCGCGGTCCAGATCAAGGCGGTCTGGAATATG 1128
DB 533 CAGGACACGAGACGCGCAACAGACACTCCCTCGCGCTCTCCACCGCGCGAGCTGT 592
QY 1129 CGGAGAGATCATGCGGTGACCAATCCGCGCGCGCATCTGTTAGGCGCGCTCGCC 1188
DB 593 CGGCAACTTCAACGCGCAAGAACCTCAGCGCGAGAGACATGGTGGTCTCTCGGCGGCA 652
QY 1189 CGCCGACATTAAACCAACCGCATTTACCGCATCTGAGACTGAAAGCTTACGACCTTC 1248
DB 653 CACCGTGGCGGCTCCCTCTCTCTCTTCAACCAACCGCTCTTACGCTTACGCAACGC 712
QY 1249 CTACGCGCGCTCCGTCTTCTCGGCTGGGCGCAAAAAGTTTGGAAAAACCAACCAT 1308
DB 713 CAGGAGAGTCAACCCACCATCAAGTTCGCTTACGCCCTCTGCTGGGCGCATTTGCC 772
QY 1309 CTGCTCTTTGGGCGCGGCAACGCGGCAAGCAACATCGGGAAGCATCGCCACGC 1368
DB 773 GTCCAAACACGACGAGTTCTTCCCAACACCAACGACATGACCTCATACGCGCGC 832
QY 1369 CGTGCCTTTACGCGTCCGCTCACTGACCAATGAGAATTTCCCTTCAACGATGGCT 1428
DB 833 GCTGTCAACAACAGTACTAGTGTGGCTGCGCCAAACCTCGGCTTTACGCTCGA 892
QY 1429 CGACAAGATGATGATC 1444
DB 893 CAGGCTCTGCTCAC 908

RESULT 9
US-10-953-349-33793
; Sequence 33793, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33793
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33793

Query Match 1.0%; Score 47; DB 6; Length 1302;
Best Local Similarity 45.6%; Pred. No. 0.0046;
Matches 204; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 1072 CTCCTTCAAGCGCGCTCAACTGCGGTCCCAATCAAGCGCGCTTGGCAATGCCG 1131
DB 489 CGCGCGCACTCAACTCCCGCGCGCGCCCAAGGAAACCGGCGTGCACCTGGCGC 548
QY 1132 CAAGATCATGCGGTGACCAATCCGCGCGCACTGATGAGGCGCGCTCGCGCGC 1191
DB 549 CGAATGATCTCC---CGAATGATGTCGTGCTTCAACAACGCGCAACCCAG 605
QY 1192 CGACATTAAACCAACCGCATTTACCGGATCTGGAGCTGAACGCTTACGACCTGCTA 1251
DB 606 CGCAGAGAGCGCTCAACGCGGTCAACCGCGCTGAGTGTCTCGAAGGCTCATAGAGTT 665
QY 1252 CGCGGCTCGCTTTCTTCTGCGGTGGCCAGAAAAGTTGGAAGAACGCAACCATTTG 1311

DB 666 CTTGTCAAGGCGCGCTGCGGGGCTCAAGCATGAGCCCAACAGCTCAAGCTCTG 725
QY 1312 GCTTTTGGGCGCGGCACCAACGCGCAAGACCAATCGGGAAGCATCGGCCAGCGCT 1371
DB 726 CTTGAGCTGTGATGATCGCGGTGATGTGACCAACGCGGACGTCAACGCGCGCGA 785
QY 1372 GCCCTTCAAGGCTGCGCTCAACTGAGCAATGAGAACTTTCCCTTCAACGATTCGTCGA 1431
DB 786 CGAGCGCGGGGAAGCAACGCGCGCGCGCGCACTTCCCAAGAGCGACCGCGAGCA 845
QY 1432 CAAGATGTGATCTGTTGGAGAGAGGCGCAAGATGACGCGCAAGGTCTGTGATCCGCA 1491
DB 846 CAGCTTGTAGCTTGAACGATGAACTCAAGCTCATATGATACAGGCGCAGAGATGGCGC 905
QY 1492 GGCATTTCTGGGCGGCGCAAGGTGCG 1518
DB 906 TGCGCGGTGCGCGCGGTGAGCGAG 932

RESULT 10
US-10-953-349-27324
; Sequence 27324, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27324
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-10-953-349-27324

Query Match 1.0%; Score 46.6; DB 6; Length 845;
Best Local Similarity 46.0%; Pred. No. 0.0047;
Matches 203; Conservative 0; Mismatches 229; Indels 9; Gaps 1;

QY 1061 GCTGTGATCTTCTTCAAGCGCGCTCCAACTCGCGGTCCAGATCAAGCGCTCTG 1120
DB 249 GACTCCAGAGTCCGCTTCAAGCGCGGAGCGAGCGGCTCGGCTCTCGCGGCGCGC 308
QY 1121 GACAAATCCGGAAGATCATGCGCTGACCAATTCGCGCGCACTGATGAGGCC 1180
DB 309 GAGCTCTTCCCGACCTGATCCGCTGCGCTCGCTCTCTCTCTCTCTCTCTCTAC 368
QY 1181 GCTCGCGCGCGCAATTAACCAACCGCATTTACCGCATCTGAGCTGAACGCTAC 1240
DB 369 CAGCAAAACGCAACTGCGCGCGCGCGCGCTTCTCTCTCGCACTCAACGACTCC 428
QY 1241 GACCTGCTTACGCGCGCTCGTCTTCTCGGCTGGGCGCGCAAAAAGTTTGGAAAAACG 1300
DB 429 GAGACCTCTCGACCTCGCGGAGTGCAGGCGCTCGCGAGCGGCTGTCAGCGCAAC 488
QY 1301 AACCACTTGGCT-----GTTTGGGCGCGCACACGCGGCAAGAACCAATATGCG 1351
DB 489 GCGCTGACCTGTCTGCAACAACCTCTCGGCTCTTCCGAGGTGAGCCCGGAGAGGC 548
QY 1352 GAAGCCATGCGCGCAACGCGGTGCGCTTCTACGCGTGGCTGATGAGCAATGAGAACTTT 1411
DB 549 GAGCGGTGACCAATTTCTTGGCGGTCTTGAAGACTTATGACCTTCGCGCGCACTC 608
QY 1412 CCTTCAAGATTTGCTGCAACAGATGTATGTTGGAGAGAGGCAAGATGACGCGC 1471
DB 609 GCGACCTCTGTGTGACCGCACCAAGGTCTCGGAGGCTGCTGCGCGCGCTCAAGGCC 668
QY 1472 AAGTGTGAGTCCGCAAG 1492
DB 669 CGGACTTGAAGGCCAACAG 689

RESULT 11

US-10-513-348-6
Sequence 6, Application US/10513348
Publication No. US20060093589A1
GENERAL INFORMATION:
APPLICANT: Warington, Kenneth H.
APPLICANT: Muzyczka, Nicholas
TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR
FILE REFERENCE: 4300,016100
CURRENT APPLICATION NUMBER: US/10/513,348
CURRENT FILING DATE: 2004-10-29
PRIOR APPLICATION NUMBER: PCT/US04/05205
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: PCT/US03/13583
PRIOR FILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-513-348-6

Query Match 1.0%; Score 45; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2889 TGGCATTGCGATTCCACATGCTGGGCGACAGATCATACCAACC 2933
DB 1 TGGCATTGCGATTCCACATGCTGGGCGACAGATCATACCAACC 45

RESULT 12

US-10-953-349-38921
Sequence 38921, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38921
LENGTH: 2152
TYPE: DNA
ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

Query Match 0.9%; Score 43.6; DB 6; Length 2152;
Best Local Similarity 42.6%; Pred. No. 0.048;
Matches 284; Conservative 0; Mismatches 379; Indels 3; Gaps 1;

QY 999 TGGTGGGTGGCTGTGAGCCGGGCGATCACTCCGAGAGAGATCCAGAGAGACC 1058
DB 412 TGTATCCGGGCTCCGGCGACAAAGCCCATGATGCGGGGTGCACTTCAAGGGCGAGAGAAC 471
QY 1059 AGGCTGTATACATCTCTTCAAGCGCGCTCCAACTCGGGTCCAGATCAAGCGCTC 1118
DB 472 AGTTCTCGCGCGAGAGATCAAGCTCCATGATCTCTGAACAAGATGAAGAGAGCGCGAGG 531
QY 1119 TGGAAATGCGCGGCAAGATCAAGGCGCTGACCAATCCGGCGCGCATTAACCTGTAGGCC 1178
DB 532 CTTACTCTGGGACCAACCATCAAGAAAGCTGTGTGTCACCGTCCGGGCTTAATTCAAGCACT 591
QY 1179 CCGCTCCGCGCGACATTAACCAACCGCATTTACCGCATCTGTGAGGTGAAGCGCT 1238

DB 592 CCCAGCGCAGGCGCACAGAGACGGCGGCTGATCTCCGGCGCTCAACGTCAATGCCATCA 651

QY 1239 AGACCTGCTCTACGCGCGCTCCGCTCTTCTGCGTGGGCCCAAGAAAGTTCCGAAAC 1298

DB 652 TCAAGAGACCCACCGCCCGGCGCATGCAATCGGGCTCGAACAAGATGAGACAGCGACG 711

QY 1239 GCAACACCATCTGGCTGTTTGGGCGCGGCGACACAGGGGCAAGCAACAATCGCGAAGCA 1358

DB 712 GCGAAGAAAGTCTCTCATCTTCCACTTCGGGCGGGGTAACCTTTACGCTTCTGCTCTCA 771

QY 1359 TCGCCACGCGTGCCCTTCTACGCGCTGCTCACTGAGCAATGAGAACTTTCCTTCA 1418

DB 772 CCATGAGAGAGGAGCATTTTGAAGTCAAGGCAACGCGCGGCGACACCCACCTCGGAGGCG 831

QY 1419 ACGATTGCTGACAAAGATGATGTGTGTGG--AGAGAGCAAGATGACGCGCAAG 1475

DB 832 AGGACTTGACAAACGCGCTGTGAAACAATTGTCAGAGAGTTCAAGAGAAAGAACGA 891

QY 1476 TGTGAGATCGCGCAAGGCAATTCTCGCGGCGAGCAAGTGCGCGGTGAGCAAAAGTCA 1535

DB 892 AGGACATACCTGGCAACCCCAAGGCGCTTCGCGACTAGAACGCTGCGAGAGGCTA 951

QY 1536 AGTCGTCCGCCAGATGATCCACCCCGTGATGTCACCTCCAACAACATGTGCG 1595

DB 952 AGAGAGCGCTCTCCCTCCACCGCGCAACACCATGAGATGAGTGGCTTATAGAGGCA 1011

QY 1596 CCGTATGAGGAGGAACGACACACCTTTCAGACACACAGCCGTTGACAGACCGGATGT 1655

DB 1012 TCGACTTCTTAACGACCATCAACCGTGCCGCTTCGAGAGCTCAACATGACCTTCC 1071

QY 1656 TCAAT 1661
DB 1072 GCAAGT 1077

RESULT 13

US-10-953-349-32310
Sequence 32310, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32310
LENGTH: 1439
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-953-349-32310

Query Match 0.9%; Score 43.4; DB 6; Length 1439;
Best Local Similarity 50.2%; Pred. No. 0.044;
Matches 107; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 1312 GCTGTTTGGGCGGCGACCAAGGCAAGCAATCGCGGAAGCATCGGCCACGCCGT 1371
DB 232 GCTGTGGCGCTGTGTCGGGCGGACGCGGCGACAGACAGCGGTGTGCGCGGATGCT 291
QY 1372 GCCCTTACGCGCTGCTGCACTGGAACCAATGAGAACTTTCCCTTCAAGATGCGTGA 1431
DB 292 GTTCTGCAACCAAGTGAAGAGACGGCGCGCTCTTCACTTAACCGCTTACCGGGC 351
QY 1432 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
DB 352 GCGGTGCGATTCAGATGCGGCGGCGGCGGACACCCCAATCAAGGTGCGGATGACAC 411
QY 1492 GGCATTTCTCGCGGCAAGGATGCGGTGA 1524

Db 412 CAACGTGTCGCGGCTTCTCCGTGCGCATGGA 444

RESULT 14

US-10-513-348-1
; Sequence 1, Application US/10513348
; Publication No. US20060093589A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, Kenneth H.
; APPLICANT: Opie, Shaun R.
; APPLICANT: Muzyczka, Nicholas
; TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 4300.016100
; CURRENT APPLICATION NUMBER: US/10/513,348
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: PCT/US04/05205
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/13583
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-513-348-1

Query Match 0.9%; Score 43.2; DB 6; Length 48;
Best Local Similarity 93.8%; Pred. No. 0.0091;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2194 GACTTAACCGATGCTGCTGCCATGCTTATCTTCAGATTGGCTCG 2241
Db 1 GATTTAATCAGTCTGCTGCCATGCTTATCTTCAGATTGGCTCG 48

RESULT 15

US-10-984-694-2
; Sequence 2, Application US/10984694
; Publication No. US20060093679A1
; GENERAL INFORMATION:
; APPLICANT: TSIEH, Roger Y.
; APPLICANT: WANG, lei
; TITLE OF INVENTION: METHODS FOR ENGINEERING POLYPEPTIDE
; TITLE OF INVENTION: VARIANTS VIA SOMATIC HYPERMUTATION AND POLYPEPTIDES MADE
; FILE REFERENCE: 39754-0976A US
; CURRENT APPLICATION NUMBER: US/10/984,694
; CURRENT FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding the fluorescent protein
; OTHER INFORMATION: mRFP1.2
US-10-984-694-2

Query Match 0.9%; Score 43.2; DB 6; Length 681;
Best Local Similarity 44.5%; Pred. No. 0.034;
Matches 171; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 1018 CCGGGGATCACTCCGAGAAAGATGATCCAGAGAGCCAGGCTGTACATCTCCTT 1077
Db 162 CCGGCTTCCGCTGGGATCTGTCTCCCAAGTTATGATGAGGCTCAAGGCTACGT 221
QY 1078 CAAGCCGCTTCAACTGCGGCTCCAGATCAAGGCCGCTTGACAAATGCGGCAAGAT 1137
Db 222 GAAGCAACCCCGCAGATCCCGACTACTGAAGCTGTCTTCCCGAGGCTTCAAGTG 281

QY 1138 CANGGCGTGAACCAATCCGGGCGCCGACTACTGTAGGCGCCGCTCCGCCCGGACAT 1197
Db 282 GGAGCGGTGATGAACTTCCAGAGACGGCGGTGTGTACCGTGAACCCAGACTCTCCCT 341
QY 1198 TAAACCAACCGCATTTTACCGCATCTGAGCTGAAAGGCTTACGACCTTGCTTACGCGG 1257
Db 342 GCAGGACGGGAGTTTATCTTACAAAGTGAAGCTGCGGACCAAACTTCCCTCCGACGG 401
QY 1258 CTCGCTTTTCTCGGCTGGGCGCCGAAAAGTTTCGAAAACGCAACCACTGTGCTGT 1317
Db 402 CCCGTAATGCAAGAAAGACCATGCGTGGAGGCTCTCTCGAGCGATGATCCCGA 461
QY 1318 TGAGCGGCGCAACCAAGACCAATGCGGAGGCGCCAGCGCGCTGCGCTT 1377
Db 462 GGAGCGGCGCTTGAAGGCGAGATCAAGATGAGCTTAAGTGAAGACCGGCGCACTA 521
QY 1378 CTACGCTGCTGCTCAACTGACCA 1401
Db 522 CGAGCGGAGGTCAAGACCACTTA 545

Search completed: June 13, 2006, 13:22:07
Job time : 152 secs

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 12:06:09 ; Search time 2682 Seconds
(without alignments)
12174.139 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683

Sequence: 1 ttggccactcctccctctgcg.....cgcatagaggagtgccaa 4683

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: _geneseqn1990s:*
- 3: _geneseqn2000s:*
- 4: _geneseqn2001as:*
- 5: _geneseqn2001bs:*
- 6: _geneseqn2002as:*
- 7: _geneseqn2002bs:*
- 8: _geneseqn2003as:*
- 9: _geneseqn2003bs:*
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- 11: _geneseqn2003ds:*
- 12: _geneseqn2004as:*
- 13: _geneseqn2004bs:*
- 14: _geneseqn2005s:*
- 15: _geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4663.8	99.6	4683	4	AAf23749 AAV6 DNA
2	4663.8	99.6	4683	10	ADL13983 Adeno-ss
3	4663.8	99.6	4683	12	ADG39763 AAV-6 gen
4	4253.2	90.8	4718	3	AAAD00772 Adeno-ss
5	4253.2	90.8	4718	10	ADe76507 Adeno-ss
6	4253.2	90.8	4718	10	ADL13984 Adeno-ss
7	4253.2	90.8	4718	12	ADG39758 AAV-1 gen
8	3831.4	81.8	4239	13	ADN39402 Adeno-ss
9	3831.4	81.8	4239	14	ADZ46598 HSV-AAV s
10	3802	81.2	4347	13	ADW39398 Adeno-ss
11	3802	81.2	4347	14	ADZ46594 HSV-AAV s
12	3802	81.2	4347	14	AEF81093 Adeno-ss
13	3678.4	78.5	4721	12	ADG39764 AAV-7 gen
14	3678.4	78.5	4721	12	ADG39764 AAV-7 gen
15	3678.4	78.5	4721	14	ADV67509 Nucleotid
16	3678.4	78.5	4721	14	ADZ27030 Adeno-ss
17	3443.2	73.5	4382	9	ABO80410 AAV9 rep
18	3404.6	72.7	4385	10	ADe76506 Adeno-ss

19	3370.4	72.0	4393	9	ACF05811 Adeno-ss
20	3370.4	72.0	4393	10	ADe76505 Adeno-ss
21	3370.4	72.0	4393	12	ADG39765 AAV-8 gen
22	3370.4	72.0	4393	14	ADV67510 Nucleotid
23	3370.4	72.0	4393	14	ADZ27032 Adeno-ss
24	3296.2	70.4	4679	4	AAI66974 Adeno-ss
25	3296.2	70.4	4679	6	ABK89694 Adeno-ss
26	3296.2	70.4	4679	10	ABV76133 Adeno-ss
27	3296.2	70.4	4679	14	AEA48850 Bovine ad
28	3296.2	70.4	4698	4	AAH26325 wild-type
29	3294.6	70.4	4679	4	AAH26325 wild-type
30	3285	70.1	4679	12	ADG39757 AAV-2 gen
31	3270.8	69.8	4680	2	AAAT09008 wild-type
32	3270.8	69.8	4680	2	ABX14497 wild-type
33	3270.8	69.8	4680	9	ADA50070 Adeno-ss
34	3270.8	69.8	4680	10	ADe81075 Adeno-ss
35	3270.8	69.8	4680	12	ADG92079 wild-type
36	3270.8	69.8	4680	14	AEH48083 Adeno-ss
37	3244.2	69.3	4675	4	AAH41481 Nucleotid
38	3244.2	69.3	4675	4	AAH41481 Nucleotid
39	3244.2	69.3	4675	6	ABA02989 Adeno-ss
40	3244.2	69.3	4675	6	ABG69879 Human ade
41	3244.2	69.3	4675	6	ABG69880 Human ade
42	3244.2	69.3	4675	10	ADe76508 Adeno-ss
43	3244.2	69.3	4675	15	AEF10041 Adeno-ss
44	3244.2	69.3	4675	15	AEF10040 Adeno-ss
45	3182.8	68.0	4722	4	AAf23748 AAV3B DNA

ALIGNMENTS

RESULT 1

AAf23749
ID AAF23749 standard; DNA; 4683 BP.

XX
XX AAF23749;

XX
XX 28-MAR-2001 (first entry)

XX
XX AAV6 DNA sequence.

XX
XX AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;
XX
XX atherosclerosis; sickle cell anemia; thalassemia;
XX
XX blood clotting disorder; diabetes; ss.

XX
XX Adeno associated virus.

XX
XX US6156303-A.

XX
XX 05-DEC-2000.

XX
XX 11-JUN-1997; 97US-00873168.

XX
XX 11-JUN-1997; 97US-00873168.

XX
XX (UNITW) UNIV WASHINGTON.

XX
XX Russell DW, Rutledge EA;

XX
XX WPI; 2001-060164/07.

XX
XX Adeno-associated virus serotype 6 and viral vector derived from it for
XX
XX gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
XX
XX syndrome, sickle cell anemia, thalassemia and diabetes.

XX
XX Claim 1; Fig 1; 50pp; English.

XX
XX The present invention relates to adeno-associated virus serotypes. The
XX
XX present sequence is the DNA sequence of one such serotype (AAV6). AAV6
XX
XX can be used to construct AAV viral vectors for use in gene therapy for a
XX
XX range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,
XX
XX sickle cell anaemia, thalassemia, blood clotting disorders and diabetes.

CC The AAV viral vectors have increased transduction efficiency of a
CC particular host cell as the AAV virion containing the AAV vector genome
CC can be modified to express a capsid protein of an AAV serotype that
CC transduces the selected host cell

XX Sequence 4683 BP, 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

Query Match 99.6%; Score 4663.8; DB 4; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
QY 1 TTGSCCACTCCCTCTCTGCGGCTTCGCTGCTCACTGAGGCCGGCGAACAAAGGTGCGC 60
Db 1 TTGGCACTCCCTCTCTGCGGCTTCGCTGCTCACTGAGGCCGGCGAACAAAGGTGCGC 60
QY 61 CGAGGCCCGGGCTTTGCCCCGGGCGCTTCAGTGAACCGACCGACCGCGAAGAGAGATG 120
Db 61 CGAGCGCCCGGGCTTTGCCCCGGGCGCTTCAGTGAACCGACCGACCGCGAAGAGAGATG 120
QY 121 GCCAACTCATCACTAGAGGGTTCTGAGAGGGTGAAGTCACTGACGTGAATTACGTCATAG 180
Db 121 GCCAACTCATCACTAGAGGGTTCTGAGAGGGTGAAGTCACTGACGTGAATTACGTCATAG 180
QY 181 GGTTAGAGAGGTCTCTGATATAGAGTCACTGAGTGTGTTGCGACATTTTSCGACACCAT 240
Db 181 GGTTAGAGAGGTCTCTGATATAGAGTCACTGAGTGTGTTGCGACATTTTSCGACACCAT 240
QY 241 GTGTCACGCTGGGTATTTAAGCCCGAGTGAACACGCGAGGTTCTCATTTGGAAGCGGGA 300
Db 241 GTGTCACGCTGGGTATTTAAGCCCGAGTGAACACGCGAGGTTCTCATTTGGAAGCGGGA 300
QY 301 GGTTTGAACGCGACGCGCATGCGAGGGTTTTCAGATTGTGATTTAAGTCCCCAGCGA 360
Db 301 GGTTTGAACGCGACGCGCATGCGAGGGTTTTCAGATTGTGATTTAAGTCCCCAGCGA 360
QY 361 CTTTGACGAGCATCTGCCCGGCATTTTCTGACAGCTTTGTGAATGAGTGGCGCGAAGGA 420
Db 361 CTTTGACGAGCATCTGCCCGGCATTTTCTGACAGCTTTGTGAATGAGTGGCGCGAAGGA 420
QY 421 ATGGAGAGTTGCGCGCAGATTCTGACATGAGATCTGAATTGAATTGACGAGGAAACCCGAC 480
Db 421 ATGGAGAGTTGCGCGCAGATTCTGACATGAGATCTGAATTGAATTGACGAGGAAACCCGAC 480
QY 481 CGTGGCGAGAGAGTGCAGCGCGACTTCTGCTGCTCACTGCGCGCGCGTGAATAGGCCCC 540
Db 481 CGTGGCGAGAGAGTGCAGCGCGACTTCTGCTGCTCACTGCGCGCGCGTGAATAGGCCCC 540
QY 541 GGAAGCCCTCTTCTTTGTTCACTGAGTGAAGAGGGCGAGTCTTAATTCCACTTCAATTCT 600
Db 541 GGAAGCCCTCTTCTTTGTTCACTGAGTGAAGAGGGCGAGTCTTAATTCCACTTCAATTCT 600
QY 601 GGTGAGAGCAACGGGGGTCAAAATCCATGATGATGCTGGGCGGCTTCCGAGTCAAGATTAGGA 660
Db 601 GGTGAGAGCAACGGGGGTCAAAATCCATGATGATGCTGGGCGGCTTCCGAGTCAAGATTAGGA 660
QY 661 CAAGCTGTGACAGCATCTACCGCGGAGATGAGCGACCTTGCCCACTGCTTCCGCGT 720
Db 661 CAAGCTGTGACAGCATCTACCGCGGAGATGAGCGACCTTGCCCACTGCTTCCGCGT 720
QY 721 GACCAAGACGCGTATGAGCGCGGAGAGGGGGGAACAAGTGTGGAACGAGTCTACATCC 780
Db 721 GACCAAGACGCGTATGAGCGCGGAGAGGGGGGAACAAGTGTGGAACGAGTCTACATCC 780
QY 781 CAACTAACCTCTGCGCAAGACTCAAGCCCGAGCTGACAGTGGCGGTGATACATAGAGGA 840
Db 781 CAACTAACCTCTGCGCAAGACTCAAGCCCGAGCTGACAGTGGCGGTGATACATAGAGGA 840
QY 841 GTATATAGCGCGTGTAAACCTGCGACGCAACGCGTCTGCGCGACGACCTGAC 900
Db 841 GTATATAGCGCGTGTAAACCTGCGACGCAACGCGTCTGCGCGACGACCTGAC 900
QY 901 CCAGTCAAGCCAGACCGAGAGCAAGAACAGAGATTTGAACCCCAATTGACGCGCC 960
Db 901 CCAGTCAAGCCAGACCGAGAGCAAGAACAGAGATTTGAACCCCAATTGACGCGCC 960
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Db 901 CCAAGTCAGCGACGCCAGAGAGCAAGAACAGAGATTTGAACCCCAATTGACGCGCC 960
QY 961 TGTATCCGGTCAAAAACCTCCGACGCTACATGAGACTGTGGGGGTGGTGGAGCG 1020
Db 961 TGTATCCGGTCAAAAACCTCCGACGCTACATGAGACTGTGGGGGTGGTGGAGCG 1020
QY 1021 GGGCATCACTCCGAGAGAGATGATCCAGAGAGACAGGCTCTGATACATCTCTTCAA 1080
Db 1021 GGGCATCACTCCGAGAGAGATGATCCAGAGAGACAGGCTCTGATACATCTCTTCAA 1080
QY 1081 CGCCGCTTCAACTCTCGGCTGCCAGATCAAGCCGCTCTGAGACATGCGCGCAAGATCAT 1140
Db 1081 CGCCGCTTCAACTCTCGGCTGCCAGATCAAGCCGCTCTGAGACATGCGCGCAAGATCAT 1140
QY 1141 GGGCTGACAAATCCGGGCGGACTCACTGATGAGGCGCGCTCCGCGCGCATTTAA 1200
Db 1141 GGGCTGACAAATCCGGGCGGACTCACTGATGAGGCGCGCTCCGCGCGCATTTAA 1200
QY 1201 AACCAACCGCATTTACCGCATCTCTGAGCTGAACCGGCTACGACCTTACCGCGGCTC 1260
Db 1201 AACCAACCGCATTTACCGCATCTCTGAGCTGAACCGGCTACGACCTTACCGCGGCTC 1260
QY 1261 GGTCTTTCTGCGCTGGGCCCAAGAAAGTTGCGAAAACGACACCATCTGCTGTTGG 1320
Db 1261 GGTCTTTCTGCGCTGGGCCCAAGAAAGTTGCGAAAACGACACCATCTGCTGTTGG 1320
QY 1321 GCGGCGCACACGAGGCGCAACCAATCGGGAAGCCATGCGCCAGCGGCTTCTA 1380
Db 1321 GCGGCGCACACGAGGCGCAACCAATCGGGAAGCCATGCGCCAGCGGCTTCTA 1380
QY 1381 CGGCTGCGTCAACTGACCAATGAGAACTTTCCCTTCAACGATTTGCTGACAAAGATGT 1440
Db 1381 CGGCTGCGTCAACTGACCAATGAGAACTTTCCCTTCAACGATTTGCTGACAAAGATGT 1440
QY 1441 GATCTGTTGGAGAGAGGCGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCTTCT 1500
Db 1441 GATCTGTTGGAGAGAGGCGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCTTCT 1500
QY 1501 CGGCGGAGCAAGGTGGCGGTGACCAAAAGTGAAGTCTGCGCCAGATCGATCCAC 1560
Db 1501 CGGCGGAGCAAGGTGGCGGTGACCAAAAGTGAAGTCTGCGCCAGATCGATCCAC 1560
QY 1561 CCCCGTATGTCATCCTTCAACACCAACATGTGCGCGGTGATTTGACGGGAAACGACACAC 1620
Db 1561 CCCCGTATGTCATCCTTCAACACCAACATGTGCGCGGTGATTTGACGGGAAACGACACAC 1620
QY 1621 CTTGAGACACACAGACGCTTTGACAGACCGGATGTTCAAAATTGAACTCACCCGCGTCT 1680
Db 1621 CTTGAGACACACAGACGCTTTGACAGACCGGATGTTCAAAATTGAACTCACCCGCGTCT 1680
QY 1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
Db 1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
QY 1741 GGATCAGTGAACCGAGGTGCGCATGAGTTCATAGTCAGAAAGGTGAGACCAACAGAG 1800
Db 1741 GGATCAGTGAACCGAGGTGCGCATGAGTTCATAGTCAGAAAGGTGAGACCAACAGAG 1800
QY 1801 ACCCGCCCCGATGACCGCGATTAAGACGAGCCCAAGCGGGCTTCCCTCATGTCGGGA 1860
Db 1801 ACCCGCCCCGATGACCGCGATTAAGACGAGCCCAAGCGGGCTTCCCTCATGTCGGGA 1860
QY 1861 TCCATGACGTCAGAGCGCGAAGAGTCCGATGAGACTTTGCGGACAGTACCAAAACAA 1920
Db 1861 TCCATGACGTCAGAGCGCGAAGAGTCCGATGAGACTTTGCGGACAGTACCAAAACAA 1920
QY 1921 ATGTTCTGTCACGCGGCGCATGCTTCAAGTGTGTTCCCTGCAAAACATGCGAGAGAT 1980
Db 1921 ATGTTCTGTCACGCGGCGCATGCTTCAAGTGTGTTCCCTGCAAAACATGCGAGAGAT 1980
QY 1981 GAATCAAAATTTCAACATTTGCTTCAAGCACGGGACCAAGAGACTGTTCAAAATGTTTCCC 2040
Db 1981 GAATCAAAATTTCAACATTTGCTTCAAGCACGGGACCAAGAGACTGTTCAAAATGTTTCCC 2040
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OY 2041 CGGCGTGCAGAACTCTCAACCGGTGTCGAGAAAGAGAGCGTATCGGAAACTCTGNGCAT 2100
DB 2041 CGGCGTGCAGAACTCTCAACCGGTGTCGAGAAAGAGAGCGTATCGGAAACTCTGNGCAT 2100
OY 2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGTCTGGCTCGCTCGATCTGCTCAACGT 2160
DB 2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGTCTGGCTCGCTCGATCTGCTCAACGT 2160
OY 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAACCAAGTATGCTGCGATG 2220
DB 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAACCAAGTATGCTGCGATG 2220
OY 2221 GTTATCTTCCAGATTGGCTCGAGACAACTCTCGAGAGGGCAATTGGGAGGTGGGACT 2280
DB 2221 GTTATCTTCCAGATTGGCTCGAGACAACTCTCGAGAGGGCAATTGGGAGGTGGGACT 2280
OY 2281 TGAACCTGGAGCCCGAAGCCCAAGCCCAACAGCAAAAGCAGAGCAGCGCCGGGGTC 2340
DB 2281 TGAACCTGGAGCCCGAAGCCCAAGCCCAACAGCAAAAGCAGAGCAGCGCCGGGGTC 2340
OY 2341 TGGTCTTCTTGGCTACAAATGCTCTGGAACCTTCAACGGACTCGACAAAGGGGAGCCG 2400
DB 2341 TGGTCTTCTTGGCTACAAATGCTCTGGAACCTTCAACGGACTCGACAAAGGGGAGCCG 2400
OY 2401 TCAACCGCGCGAGTCGACAGCGCCCTCGAGCAGCAAGAGCCCTACGACCAAGAGCTCAAG 2460
DB 2401 TCAACCGCGCGAGTCGACAGCGCCCTCGAGCAGCAAGAGCCCTACGACCAAGAGCTCAAG 2460
OY 2461 CGGCGTCAATCCGTAACCTGCGGTATTAACCAAGCCGAGCCGAGTTCAGAGAGCTGTC 2520
DB 2461 CGGCGTCAATCCGTAACCTGCGGTATTAACCAAGCCGAGCCGAGTTCAGAGAGCTGTC 2520
OY 2521 AAGAAATACGTCTTTTGGGGGCAACCTCGGGCAGAGCTTTCAGAGCCCAAGAGAGG 2580
DB 2521 AAGAAATACGTCTTTTGGGGGCAACCTCGGGCAGAGCTTTCAGAGCCCAAGAGAGG 2580
OY 2581 TTCTCGAACCTTTTGTGTGTGTGTGAGGAGGTGCTAAGCGGCTCTGAGAAAGAAACCTC 2640
DB 2581 TTCTCGAACCTTTTGTGTGTGTGTGAGGAGGTGCTAAGCGGCTCTGAGAAAGAAACCTC 2640
OY 2641 CGGTAGAGCAGTCGCAAGAGCCAGACTCCTCTCGGGCAATTGGCAAGACAGGCCAGC 2700
DB 2641 CGGTAGAGCAGTCGCAAGAGCCAGACTCCTCTCGGGCAATTGGCAAGACAGGCCAGC 2700
OY 2701 AGCCCGTAAAAAGAGACTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760
DB 2701 AGCCCGTAAAAAGAGACTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760
OY 2761 CACAACTCTGGAGAACCTTCCAGAACCTTCCAGAACCTTCCAGAACCTTCCAGAACCTT 2820
DB 2761 CACAACTCTGGAGAACCTTCCAGAACCTTCCAGAACCTTCCAGAACCTTCCAGAACCTT 2820
OY 2821 CAGCGGTGTGGCAGCAATGCGAGCAATTAAGAGGCGCGAGCGAGTGGGTATGCT 2880
DB 2821 CAGCGGTGTGGCAGCAATGCGAGCAATTAAGAGGCGCGAGCGAGTGGGTATGCT 2880
OY 2881 CAGAAATTGGCAATTGCAATTCACATGCTGTGGGAGAGAGTCAACCAAGCACCC 2940
DB 2881 CAGAAATTGGCAATTGCAATTCACATGCTGTGGGAGAGAGTCAACCAAGCACCC 2940
OY 2941 GAAATGGGCGCTTGGCCCACTTAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC 3000
DB 2941 GAAATGGGCGCTTGGCCCACTTAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC 3000
OY 3001 CGGGGGCAGCAAGCAACCACTACTTGGGCTACAGACCCCTGGGGGTATTTTGAAT 3060
DB 3001 CGGGGGCAGCAAGCAACCACTACTTGGGCTACAGACCCCTGGGGGTATTTTGAAT 3060
OY 3061 TCAACAGATTCCACTGCAATTTCTACCAAGTGTGAGAGGAGTCAATCAACCAATTT 3120
DB 3061 TCAACAGATTCCACTGCAATTTCTACCAAGTGTGAGAGGAGTCAATCAACCAATTT 3120

OY 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGTCTTTCAACATCCAAAGTCAAGAGGCTCA 3180
DB 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGTCTTTCAACATCCAAAGTCAAGAGGCTCA 3180
OY 3181 CGACGAATGATGGGCTCAAGCAATGCTAATAACCTTACAGACGGTTCAAGTCTTGT 3240
DB 3181 CGACGAATGATGGGCTCAAGCAATGCTAATAACCTTACAGACGGTTCAAGTCTTGT 3240
OY 3241 CGGACTCGGAATACCAATGCTCCCGTACGCTCTGGGCTCTGGGCAACAGAGGCTCTCTC 3300
DB 3241 CGGACTCGGAATACCAATGCTCCCGTACGCTCTGGGCTCTGGGCAACAGAGGCTCTCTC 3300
OY 3301 CGTTCCCGCGGAGCGTGTCTTGAATTCGCGAGTACGAGTACCTAACGCTCAACATGAGCA 3360
DB 3301 CGTTCCCGCGGAGCGTGTCTTGAATTCGCGAGTACGAGTACCTAACGCTCAACATGAGCA 3360
OY 3361 GCCAGGAGTGGGAGCGTCAATCTTTTATCTGCTGGAATATTTCCATCGCAGATGCTGA 3420
DB 3361 GCCAGGAGTGGGAGCGTCAATCTTTTATCTGCTGGAATATTTCCATCGCAGATGCTGA 3420
OY 3421 GAACGGGCAATTAATCTTACCTTACGCTACACCTTGAAGAGAGTGTCTTCCAGACAGCT 3480
DB 3421 GAACGGGCAATTAATCTTACCTTACGCTACACCTTGAAGAGAGTGTCTTCCAGACAGCT 3480
OY 3481 ACGGCAACAGCCAGAGCGCTGAGCCGGGTGATTAATCTCTCATGAGCCAGTACCTGATTT 3540
DB 3481 ACGGCAACAGCCAGAGCGCTGAGCCGGGTGATTAATCTCTCATGAGCCAGTACCTGATTT 3540
OY 3541 ACTGGAACAGAACTCACAAATCAATCGTCCGGAAGTGGCCAAACCAAGACTTGTATTAGCC 3600
DB 3541 ACTGGAACAGAACTCACAAATCAATCGTCCGGAAGTGGCCAAACCAAGACTTGTATTAGCC 3600
OY 3601 GTGGGTCTCCAGCTGGGCTGTCTGTTACGCCAAATACTGGCTACCTGAGACCTGTTACC 3660
DB 3601 GTGGGTCTCCAGCTGGGCTGTCTGTTACGCCAAATACTGGCTACCTGAGACCTGTTACC 3660
OY 3661 GGGGGTCTCCAGCTGGGCTGTCTGTTACGCCAAATACTGGCTACCTGAGACCTGTTACC 3720
DB 3661 GGGGGTCTCCAGCTGGGCTGTCTGTTACGCCAAATACTGGCTACCTGAGACCTGTTACC 3720
OY 3721 GTGCTTCAAAATATTAACCTTATGAGGCGTGAATCTATATCAACCTGGCACTGCTATGG 3780
DB 3721 GTGCTTCAAAATATTAACCTTATGAGGCGTGAATCTATATCAACCTGGCACTGCTATGG 3780
OY 3781 CCTCACACAAAGAGCAAGAAACAAGTCTTCCCATGAGGCGGTGCTATGTTTTTGGAA 3840
DB 3781 CCTCACACAAAGAGCAAGAAACAAGTCTTCCCATGAGGCGGTGCTATGTTTTTGGAA 3840
OY 3841 AGGAGAGGCGCGGCTTCAAAACACTGATTTGACCAATGTGATGTCACAGAGAGAGG 3900
DB 3841 AGGAGAGGCGCGGCTTCAAAACACTGATTTGACCAATGTGATGTCACAGAGAGAGG 3900
OY 3901 AAATCAAGCCACTTAACCCCTGGGCCACCGAAGATTTGGGACTGTGGCACTCAATCTCC 3960
DB 3901 AAATCAAGCCACTTAACCCCTGGGCCACCGAAGATTTGGGACTGTGGCACTCAATCTCC 3960
OY 3961 AGAGCAGAGCAGACAGACCTTGGCAGCCGAGATGTGCAATGTATGTGGAGCTTACCTGAA 4020
DB 3961 AGAGCAGAGCAGACAGACCTTGGCAGCCGAGATGTGCAATGTATGTGGAGCTTACCTGAA 4020
OY 4021 TGTGTGGCAAGACAGAGAGCTAATACCTGACAGGGTCTTATTTGGGCCAAATTTCTCA 4080
DB 4021 TGTGTGGCAAGACAGAGAGCTAATACCTGACAGGGTCTTATTTGGGCCAAATTTCTCA 4080
OY 4081 CGGATGACACTTTTCAACCCGCTCTCTCTCATGAGGCGGGCTTTGACTTAAGACCCGCTC 4140
DB 4081 CGGATGACACTTTTCAACCCGCTCTCTCTCATGAGGCGGGCTTTGACTTAAGACCCGCTC 4140
OY 4141 CTGAGATCTCATCAAAAACAAGCTGTCTCTGGAATTCCTCGGCAAGATTTTGGCTA 4200
DB 4141 CTGAGATCTCATCAAAAACAAGCTGTCTCTGGAATTCCTCGGCAAGATTTTGGCTA 4200
OY 4201 CAAAGTTTGTCTTCAATCATCAACCAATTCACAGAGCAAGTGTGAGTGAAT 4260

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Db 4201 CAAAGTTGCTTCATTCATCACCCAGTATTCACAGGACAGTAGCGGTGAGATTGAAAT 4260
Qy 4261 GGGAGCTGCAGAAAAGAAAACAGCAACCTGTGAATCCCGAAGTGCAGATATCATCTAACT 4320
Db 4261 GGGAGCTGCAGAAAAGAAAACAGCAACCTGTGAATCCCGAAGTGCAGATATCATCTAACT 4320
Qy 4321 ATGCAAAATCTGCCAAGCTTATTTCACTGTGAGCAACATGAGACTTTATATCTAGAGCTC 4380
Db 4321 ATGCAAAATCTGCCAAGCTTATTTCACTGTGAGCAACATGAGACTTTATATCTAGAGCTC 4380
Qy 4381 GCGCCATTGGGACCCCGTTACTCAACCGTCCCTGTAAATGTGTGTTATATCAATPAACCG 4440
Db 4381 GCGCCATTGGGACCCCGTTACTCAACCGTCCCTGTAAATGTGTGTTATATCAATPAACCG 4440
Qy 4441 GTTAATTCGTGCGATTGTAACCTTGTGTCATGTCCTATATCTATCTATCTGACCACTA 4500
Db 4441 GTTAATTCGTGCGATTGTAACCTTGTGTCATGTCCTATATCTATCTGACCACTA 4500
Qy 4501 GCAACCGGTTACACATTAACTGTTAGTGGCGCTTCGCGAATACCCCTAGTGAAGATT 4560
Db 4501 GCAACCGGTTACACATTAACTGTTAGTGGCGCTTCGCGAATACCCCTAGTGAAGATT 4560
Qy 4561 GCCCACTCCCTCTATGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620
Db 4561 GCCCACTCCCTCTATGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620
Qy 4621 TCTGGGAGCTTTGTGTCGCGAGGCCCAACGAGCGAGCGGCGCATAGAGGAGTGGG 4680
Db 4621 TCTGGGAGCTTTGTGTCGCGAGGCCCAACGAGCGAGCGGCGCATAGAGGAGTGGG 4680
Qy 4681 CAA 4683
Db 4681 CAA 4683

RESULT 2
ADL13983 ID ADL13983 standard; DNA; 4683 BP.
XX
AC ADL13983;
XX
DT 06-MAY-2004 (first entry)
XX
DE Adeno-associated virus serotype 6 complete DNA.
XX
KW ss: cytosolic; neuroprotective; antiinflammatory; gene therapy;
KW expression construct; adeno-associated virus;
KW integration efficiency element; inverted terminal repeat; integration;
KW chromosome; cancer; lymphoma; leukemia; myeloma; neuroblastoma;
KW retinoblastoma; inflammatory disease; arthritis;
KW neurodegenerative disease.
XX
OS Adeno-associated virus 6.
XX
PN WO2003087334-A2.
XX
PD 23-OCT-2003.
XX
PF 09-APR-2003; 2003WO-US011191.
XX
PR 09-APR-2002; 2002US-0371044P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Falck-Pedersen BS, Philpott N;
XX
DR WPI; 2003-833723/77.
XX
PT New expression construct comprising a nucleic acid sequence encoding an
PT adeno-associated virus integration efficiency element, useful for
PT treating cancer e.g. lung cancer or colon cancer or inflammatory disease
PT e.g. arthritis.
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XX
PS Disclosure; SEQ ID NO 2; 62pp; English.
XX
CC The invention relates to an expression construct comprising a nucleic
CC acid sequence encoding an adeno-associated virus integration efficiency
CC element (AAV IEB), which is devoid of AAV inverted terminal repeats (AAV
CC ITRs) and site-specifically integrates into a host cell chromosome when
CC provided to the host cell in conjunction with an AAV Rep protein. The
CC expression construct can be used as a therapeutic factor for treating a
CC mammal for a pathologic state which is cancer, including lung cancer,
CC colon cancer, renal cancer, anal cancer, bile duct cancer, bladder
CC cancer, bone cancer, brain cancer, spinal chord cancer, breast cancer,
CC cervical cancer, lymphoma, endometrial cancer, esophageal cancer,
CC gallbladder cancer, gastrointestinal cancer, laryngeal cancer, leukemia,
CC liver cancer, multiple myeloma, neuroblastoma, ovarian cancer, pancreatic
CC cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer,
CC testicular cancer, thymus cancer or thyroid cancer. Other pathologic
CC state includes inflammatory disease (arthritis), neurodegenerative
CC disease, a disease of an organ attributed to the presence of increased or
CC decreased level of a particular gene product(s). This sequence
CC corresponds to the AAV serotype 6 complete DNA including the IEB
CC sequence.
XX
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
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Query Match 99.6%; Score 4663.8; DB 10; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Qy 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGCCCGGCGACCAAGGTGCGC 60
Db 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGCCCGGCGACCAAGGTGCGC 60
Qy 61 CGAGCGCCCGGCTTTGGCCCGGCGGCGCTCAGTGAAGCGAGCGCGCGACAGAGGAGTGTG 120
Db 61 CGAGCGCCCGGCTTTGGCCCGGCGGCGCTCAGTGAAGCGAGCGCGCGACAGAGGAGTGTG 120
Qy 121 GCCAATCTCATCACTAAGGGGTTCTTGAGGAGGTGAGTCTGTGACGTGAATTACGTATAG 180
Db 121 GCCAATCTCATCACTAAGGGGTTCTTGAGGAGGTGAGTCTGTGACGTGAATTACGTATAG 180
Qy 181 GGTTAGGAGAGTCTGTATTAGAGTCACTGAGTGTGTTGGCAGATTTTGGCAGACCAT 240
Db 181 GGTTAGGAGAGTCTGTATTAGAGTCACTGAGTGTGTTGGCAGATTTTGGCAGACCAT 240
Qy 241 GTGGTCAAGCGTGGGTATTTAAGCCCGAGTAGACGAGGAGGTCCCATTTTGAAGCGGGA 300
Db 241 GTGGTCAAGCGTGGGTATTTAAGCCCGAGTAGACGAGGAGGTCCCATTTTGAAGCGGGA 300
Qy 301 GATTGAAACGCGACGCGCATGCGCGGGTTTACGAGATTGTGATTAAAGTCCCAAGCGA 360
Db 301 GATTGAAACGCGACGCGCATGCGCGGGTTTACGAGATTGTGATTAAAGTCCCAAGCGA 360
Qy 361 CTTTGAAGAGCATCTGCGCGGCACTTTCTGACACTTTTGTGAATCTGGTGGCGAGAGGA 420
Db 361 CTTTGAAGAGCATCTGCGCGGCACTTTCTGACACTTTTGTGAATCTGGTGGCGAGAGGA 420
Qy 421 ATGGAGATTGCGCGCAGATTCTGACATGATCTGAATCTGATTGAGAGGACACCCCTGAC 480
Db 421 ATGGAGATTGCGCGCAGATTCTGACATGATCTGAATCTGATTGAGAGGACACCCCTGAC 480
Qy 481 CGTGCCGAGAAAGCTGACGCGGCACTTCTGTGTCACTGCGCGCGCGCTGAGTAAAGCCCC 540
Db 481 CGTGCCGAGAAAGCTGACGCGGCACTTCTGTGTCACTGCGCGCGCGCTGAGTAAAGCCCC 540
Qy 541 GAGAGCCCTCTCTTTTGTATGTTTGAAGTGAAGAGGCGAGTCTACTTCCACTCATATCT 600
Db 541 GAGAGCCCTCTCTTTTGTATGTTTGAAGTGAAGAGGCGAGTCTACTTCCACTCATATCT 600
Qy 601 GGTGAGAACCAAGGAGGTCAATTCATGATGATGAGGCGCTTCTCTGAGTCAGATTAGCGA 660
Db 601 GGTGAGAACCAAGGAGGTCAATTCATGATGATGAGGCGCTTCTCTGAGTCAGATTAGCGA 660
```

Qy 661 CAAAGTGGTGAAGACCAATCTACCGCGGATCGAGCCGACCTGTGCCAACTGGTTCGCGGT 720
Db 661 CAAAGTGGTGAAGACCAATCTACCGCGGATCGAGCCGACCTGTGCCAACTGGTTCGCGGT 720
Qy 721 GACCAAGAAGCGGTAAATGGCGCGGAGGGGGGAAACAAGGTGTGACAGAGTGTACATCC 780
Db 721 GACCAAGAAGCGGTAAATGGCGCGGAGGGGGGAAACAAGGTGTGACAGAGTGTACATCC 780
Qy 781 CAACTAACCTCTGGCCCAAGACTACACCGGAGTGAAGTGGGTGTGAATGAATGAAGA 840
Db 781 CAACTAACCTCTGGCCCAAGACTACACCGGAGTGAAGTGGGTGTGAATGAATGAAGA 840
Qy 841 GTATATAAGCGGTGTAAACCTGAGCGGACCAACCGCTGTGGCGCAAGACTGAC 900
Db 841 GTATATAAGCGGTGTAAACCTGAGCGGACCAACCGCTGTGGCGCAAGACTGAC 900
Qy 901 CCACGTCAAGCCAGACCCAGAGACAGAAACAAGAGATCTGAACCCCAATTCTGACGCGC 960
Db 901 CCACGTCAAGCCAGACCCAGAGACAGAAACAAGAGATCTGAACCCCAATTCTGACGCGC 960
Qy 961 TGTGATCCGGTCAAAAACCTCCGCAAGCTACATGAGAGTGTGGGTGGCTGTGGACCG 1020
Db 961 TGTGATCCGGTCAAAAACCTCCGCAAGCTACATGAGAGTGTGGGTGGCTGTGGACCG 1020
Qy 1021 GGGCATCACTCCGAGAAAGCATGATGATCGAGAGACCGACCTGTGATCTCTTCA 1080
Db 1021 GGGCATCACTCCGAGAAAGCATGATGATCGAGAGACCGACCTGTGATCTCTTCA 1080
Qy 1081 CGCGGCTTCAACTCGCGGTCCAGATCAAGGCGCTGTGACAAATGCGCGGAGATCAT 1140
Db 1081 CGCGGCTTCAACTCGCGGTCCAGATCAAGGCGCTGTGACAAATGCGCGGAGATCAT 1140
Qy 1141 GGGCGTGAACAAATCCGCGGCGGACCTACCTGTAGGCGCGCTCGCGCGCGGACATTAA 1200
Db 1141 GGGCGTGAACAAATCCGCGGCGGACCTACCTGTAGGCGCGCGCTCGCGCGGACATTAA 1200
Qy 1201 AACCAACCGCATTTACCGCATCTGTGAGCTGAACGGCTACGACCTGTGACCGCGGCTC 1260
Db 1201 AACCAACCGCATTTACCGCATCTGTGAGCTGAACGGCTACGACCTGTGACCGCGGCTC 1260
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Db 1321 GCCCGCCACACAGGCGCAAGACCAATGCGGAAACCATCGGCCACGCGTGTCTTA 1380
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Dh 2881 CAGGAATTTGGCATTTGGATTCCACATGGCTGGGGGAGAGAGTCATACCA CCGACACC 2940
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Dh 3421 GAACGGGCAATTAACCTTACCTTCACTACCTT GAGGAGGCTGCTTCCACAGCAGCT 3480
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Dh 4021 TGGTGTGGCAAGACAGAGCGTATACCTGCA GGGTCTTATTTGGGCCAAATTCCTACA 4080
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Dh 4081 CGGATGGACACTTTCACCGCTCTCATAGGCGG CTTTGAACCTTAACACCCGCTC 4140
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Dh 4561 GCCCACTCTCTATGCGCGCTGCTGCTGCGTGG GGGCGGCAAGACAGCTTGGCCG 4620
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Dh 4621 TCTGCGGACCTTTGGTCCGAGGCGCCACCGAG GCGAGCGGCACTAAGGGAATGGG 4680
Qy 4681 CAA 4683
Dh 4681 CAA 4683

RESULT 3
ADG39763
ID ADG39763 standard; DNA; 4683 BP.
XX
AC ADG39763;
XX
DE 11-MAR-2004 (first entry)
XX
XX AAV-6 genomic DNA sequence SEQ ID NO:25.
XX
XX parvovirus; rep; cap; DNA binding domain; capsid interacting domain;
XX
XX recombinant hybrid parvovirus particle;
XX
XX recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
XX
XX gene; ds.
XX
XX Adeno-associated virus 6.
XX
XX W02003104392-A2.

PD 18-DEC-2003.
XX 02-DEC-2002; 2002MO-US038423.
XX 18-DEC-2001; 2001US-0341919P.
XX (UNNC-) UNIV NORTH CAROLINA.
XX PA
XX Samliski RJ, Rabinowitz JE;
XX WPI; 2004-062324/06.
PT New polynucleotides comprising parvovirus rep coding sequences and
PT parvovirus cap coding sequences, useful in producing higher stocks of
PT hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
PT subject.
XX Disclosure; SEQ ID NO 25; 115bp; English.
XX
XX The present invention describes a polynucleotide (1), comprising
XX parvovirus rep coding sequences and parvovirus cap coding sequences. The
XX rep coding sequences encodes a DNA binding domain from a first
XX parvovirus, and a capsid interacting domain from a parvovirus different
XX from the first parvovirus. The cap coding sequence comprises sequences
XX from the different parvovirus. Also described: (1) a vector comprising
XX (1); (2) a cell comprising (1), or parvovirus rep coding sequences and
XX parvovirus cap coding sequences, where the rep coding sequences encode a
XX DNA binding domain from a first parvovirus and a capsid interacting
XX domain from a parvovirus different from the first parvovirus, the cap
XX coding sequences comprise sequences from the different parvovirus, and
XX the rep coding sequences are stably integrated into the genome of the
XX cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
XX -associated virus (AAV) particle. (1) can be used in vaccines, and in
XX gene therapy. The polynucleotide (1) can be used in producing higher
XX stocks of hybrid parvoviruses or parvovirus vectors, which may be used in
XX the delivery of nucleic acids having biological effect to treat or
XX ameliorate the symptoms associated with any disorder related to gene
XX expression. The polynucleotide may be used to produce a parvovirus vector
XX to express an immunogenic polypeptide in a subject, e.g. for vaccination.
XX The parvovirus vector may also be used to provide an antisense nucleic
XX acid to a cell in vitro or in vivo, or in diagnostic and screening
XX methods. The present sequence is used in the exemplification of the
XX present invention.
XX
XX Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
SQ
Query Match 99.6%; Score 4663.8; DB 12; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCCGGGCGAACAAAGTCCGC 60
DB 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCCGGGCGAACAAAGTCCGC 60
QY 61 CGAGCCCGGGGCTTGGCCCGGGCGGCTCAGTGAAGCGAGCGCGAGAGAGGAGT 120
DB 61 CGAGCCCGGGGCTTGGCCCGGGCGGCTCAGTGAAGCGAGCGCGAGAGAGGAGT 120
QY 121 GCCAATCTCATCTAGGAGGTTCTTGAAGGGTGAAGTCTGAAGTGAATACGTATAG 180
DB 121 GCCAATCTCATCTAGGAGGTTCTTGAAGGGTGAAGTCTGAAGTGAATACGTATAG 180
QY 181 GGTTAAGGAAGTCTCTGTATTTAGAGTCAAGTGAAGTCTTGGAGACATTTTGGACACAT 240
DB 181 GGTTAAGGAAGTCTCTGTATTTAGAGTCAAGTGAAGTCTTGGAGACATTTTGGACACAT 240
QY 241 GTGGTCAAGTCTGGATTTAAGCCGAGTGAAGCGAGGCTCTCATTTTGAAGCGGGA 300
DB 241 GTGGTCAAGTCTGGATTTAAGCCGAGTGAAGCGAGGCTCTCATTTTGAAGCGGGA 300
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DB 421 ATGGAGTTGGCCGAGATTTCTGACATGAGATCTGAATCTGAATTGAGCAGGACCCCTTAC 480
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DB 481 CTGGCCGAGAGAGCTGACGCGCGCACTTCTGTGTCACCTGCGCGCGGTGAGTAAAGCCCC 540
QY 541 GGAGGCCCTCTTCTTTGTTGTCAGTTGAGAAAGGGGAGTCTTCACTTCCATTTCT 600
DB 541 GGAGGCCCTCTTCTTTGTTGTCAGTTGAGAAAGGGGAGTCTTCACTTCCATTTCT 600
QY 601 GGTGAGAGACACGGGGGTCAATTCATGAGTCTGGGCGGCTTCTGAGTCAAGATTAGCGA 660
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DB 841 GTATATAAGCGCGTGTAAACCTGCGCGAGCGCAAAAGGCTGTGGCGACAGCTGAC 900
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| | | | |
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| | | | |
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| | | | |
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| | | | |
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Qy 2281 TGAACCTGGAGCCCGGAAACCAAGGCCAACAGCAAAAGAGAGAGCAAGCGCGGGCTC 2340
| | | | |
Db 2281 TGAACCTGGAGCCCGGAAACCAAGGCCAACAGCAAAAGAGAGAGCAAGCGCGGGCTC 2340
Qy 2341 TGGTGTCTTCTGTGCTACAAGTACCTCGGACCTTCAACGGACTGCAAGAGGGGAGCCCG 2400
| | | | |
Db 2341 TGGTGTCTTCTGTGCTACAAGTACCTCGGACCTTCAACGGACTGCAAGAGGGGAGCCCG 2400
Qy 2401 TCAACGCGGCGGATGCAAGCGGCTTCAGACAGACAGAGGCTTACGACAGAGCTCAAG 2460
| | | | |
Db 2401 TCAACGCGGCGGATGCAAGCGGCTTCAGACAGACAGAGGCTTACGACAGAGCTCAAG 2460
Qy 2461 CGGCGTGAATTCGCTGACGCTGCGGATTAACCAAGCGGAGCCGAGTTTCAAGAGCGTCTGC 2520
| | | | |
Db 2461 CGGCGTGAATTCGCTGACGCTGCGGATTAACCAAGCGGAGCCGAGTTTCAAGAGCGTCTGC 2520
Qy 2521 AAGAAATATCGTCTTTTGGGGCAACCTCGGGCGAGAGTCTTCCAGGCAAGAAAGGG 2580
| | | | |

Db 2521 AAGAAATATCGTCTTTTGGGGCAACCTCGGGCGAGAGTCTTCCAGGCAAGAAAGGG 2580
| | | | |
Qy 2581 TTCTCGAATCTTTTGTCTGTGTTGAGGAAGTGTCTAAGAGGCTCTCTGGAAAGAAACGTC 2640
| | | | |
Db 2581 TTCTCGAATCTTTTGTCTGTGTTGAGGAAGTGTCTAAGAGGCTCTCTGGAAAGAAACGTC 2640
Qy 2641 CGGTAGAGAGTGCAGCAAGAGCCAGACTCTCTCGGCGATTTGGCAAGACAGGCCAGC 2700
| | | | |
Db 2641 CGGTAGAGAGTGCAGCAAGAGCCAGACTCTCTCGGCGATTTGGCAAGACAGGCCAGC 2700
Qy 2701 AGCCGCTAAAGAGACTCAATTTTGTGTGACAGTGGCGACTGAGTCACTGTCGCCAGC 2760
| | | | |
Db 2701 AGCCGCTAAAGAGAGACTCAATTTTGTGTGACAGTGGCGACTGAGTCACTGTCGCCAGC 2760
Qy 2761 CACAACTCTCGAGAACTTCAGCAACCCCGCTGTGTGGGACCTCACTACATGCTT 2820
| | | | |
Db 2761 CACAACTCTCGAGAACTTCAGCAACCCCGCTGTGTGGGACCTCACTACATGCTT 2820
Qy 2821 CAGCGGTGGCGCACCAATGAGAGCAATTAAGAGGCGCGAGAGTGGTAAATGCT 2880
| | | | |
Db 2821 CAGCGGTGGCGCACCAATGAGAGCAATTAAGAGGCGCGAGAGTGGTAAATGCT 2880
Qy 2881 CAGGAAATTTGCAATTTGCAATGCTGAGTCAATGCTGAGTCAATCAACAGCACCC 2940
| | | | |
Db 2881 CAGGAAATTTGCAATTTGCAATGCTGAGTCAATGCTGAGTCAATCAACAGCACCC 2940
Qy 2941 GAACATGGGCTTGGCCCACTATTAACACCACTTCAAGCAAAATCTCCAGTCTTCA 3000
| | | | |
Db 2941 GAACATGGGCTTGGCCCACTATTAACACCACTTCAAGCAAAATCTCCAGTCTTCA 3000
Qy 3001 CGGCGGCGACCAACGACAACTACTTCCGCTTACAGCACCCCTGGGGGTATTTGAT 3060
| | | | |
Db 3001 CGGCGGCGACCAACGACAACTACTTCCGCTTACAGCACCCCTGGGGGTATTTGAT 3060
Qy 3061 TCAACAGATTCACTGCCATTTTCTCACACAGTGACTGGACGCACTCATCAACAAT 3120
| | | | |
Db 3061 TCAACAGATTCACTGCCATTTTCTCACACAGTGACTGGACGCACTCATCAACAAT 3120
Qy 3121 GGGGATTCGGGCCCAAGAGCTCAACTTCAAGGCTTCAACATTCGAAGTCAAGAGGTCA 3180
| | | | |
Db 3121 GGGGATTCGGGCCCAAGAGCTCAACTTCAAGGCTTCAACATTCGAAGTCAAGAGGTCA 3180
Qy 3181 CGAGAAATGATGGGTACAGACCACTGCTAATACTTACACAGCGTTCAGATCTTGT 3240
| | | | |
Db 3181 CGAGAAATGATGGGTACAGACCACTGCTAATACTTACACAGCGTTCAGATCTTGT 3240
Qy 3241 CGGACTGAGATACAGTTCCTCGTACGTCTCGGCTGTGCGCACAGGGCTGCTCCTC 3300
| | | | |
Db 3241 CGGACTGAGATACAGTTCCTCGTACGTCTCGGCTGTGCGCACAGGGCTGCTCCTC 3300
Qy 3301 CGTTCCCGGGGAGCTGTGATGATTCGAGTACAGGCTACCTAAGCTCAACATGAGCA 3360
| | | | |
Db 3301 CGTTCCCGGGGAGCTGTGATGATTCGAGTACAGGCTACCTAAGCTCAACATGAGCA 3360
Qy 3361 GCCAGGAGTGGAGCGCTCATCTTCTTACTGCTGGAAATTTCCATGCAATGCTGA 3420
| | | | |
Db 3361 GCCAGGAGTGGAGCGCTCATCTTCTTACTGCTGGAAATTTCCATGCAATGCTGA 3420
Qy 3421 GAAAGGCAATTAATCTTACCTTACGCTACACTTTCAGAGAGTGGCTTTCACAGAGCT 3480
| | | | |
Db 3421 GAAAGGCAATTAATCTTACCTTACGCTACACTTTCAGAGAGTGGCTTTCACAGAGCT 3480
Qy 3481 ACCGCGACAGCCAGAGCTGAGCCGCGTGTGATCCTCTACAGACAGTACTGAT 3540
| | | | |
Db 3481 ACCGCGACAGCCAGAGCTGAGCCGCGTGTGATCCTCTACAGACAGTACTGAT 3540
Qy 3541 ACCTGAACAGAACTCAATCAATCAATCGGAGAGTCCCAAAACAGAGACTTGTCTTTAGCC 3600
| | | | |
Db 3541 ACCTGAACAGAACTCAATCAATCAATCGGAGAGTCCCAAAACAGAGACTTGTCTTTAGCC 3600
Qy 3601 GTGGGTCTCAAGTGGGATGCTGTTCAGCTCCAAAACTGGCTTACCTGAGCCTGTTACC 3660
| | | | |

Db 3601 GGGGGTCTCAGCTGGCATGTCTGTTCAAGCCCAAAAATGCGTACTGGAACCTGTACC 3660
 QY 3661 GGGAGACGGGGTCTTCTTAAACAAAACAGACAAACAACAGCAACTTTACCTGGATCG 3720
 Db 3661 GGGAGACGGGGTCTTCTTAAACAAAACAGACAAACAACAGCAACTTTACCTGGATCG 3720
 QY 3721 GTGCTTCAAAATATATACCTTATGGGCGTGAATCATATATCAACCTGGACCTGCTATGG 3780
 Db 3721 GTGCTTCAAAATATATACCTTATGGGCGTGAATCATATATCAACCTGGACCTGCTATGG 3780
 QY 3781 CCTCACACAAAAGCAGACAAAGCAAGTCTTTCCCATGAGCGGTGCATGATTTTGGAA 3840
 Db 3781 CCTCACACAAAAGCAGACAAAGCAAGTCTTTCCCATGAGCGGTGCATGATTTTGGAA 3840
 QY 3841 AGGAGAGGCGGGAGCTTCAAACTACTGATTTGGACATGTATATCAACAGAGAGG 3900
 Db 3841 AGGAGAGGCGGGAGCTTCAAACTACTGATTTGGACATGTATATCAACAGAGAGG 3900
 QY 3901 AAATCAAAAGCCACTAACCCCGTGGCCAGAAAGATTGGGACTGTGCAATCTCC 3960
 Db 3901 AAATCAAAAGCCACTAACCCCGTGGCCAGAAAGATTGGGACTGTGCAATCTCC 3960
 QY 3961 AGAGCAGCAGACAGACCCCTGCGACCGAGATGTGCATGTTATGGAGCCTTACCTGGA 4020
 Db 3961 AGAGCAGCAGACAGACCCCTGCGACCGAGATGTGCATGTTATGGAGCCTTACCTGGA 4020
 QY 4021 TGGTGTGGCAGACAGACAGTATCTGCGAGGGTCTTATTTGGCCAAATTTCTCTCA 4080
 Db 4021 TGGTGTGGCAGACAGACAGTATCTGCGAGGGTCTTATTTGGCCAAATTTCTCTCA 4080
 QY 4081 CGGATGGAACCTTTCACCCGCTCTCCTCATGGGGGCTTTGGAACCCGCGCTC 4140
 Db 4081 CGGATGGAACCTTTCACCCGCTCTCCTCATGGGGGCTTTGGAACCCGCGCTC 4140
 QY 4141 CTCAGATCTCTATCAAAAACAAGCCTGTCTCTGCGAATCTCTCCGACAGATTTTGGGTA 4200
 Db 4141 CTCAGATCTCTATCAAAAACAAGCCTGTCTCTGCGAATCTCTCCGACAGATTTTGGGTA 4200
 QY 4201 CAAAGTTTGTCTTCAATTCATCCAGTATTTCAACAGACAAAGTGAAGCTGAGATTGAAT 4260
 Db 4201 CAAAGTTTGTCTTCAATTCATCCAGTATTTCAACAGACAAAGTGAAGCTGAGATTGAAT 4260
 QY 4261 GGGAGCTGCAAGAAAACAGCAAAAGCTGGAATCCGAACTGCAATCTTAATCT 4320
 Db 4261 GGGAGCTGCAAGAAAACAGCAAAAGCTGGAATCCGAACTGCAATCTTAATCT 4320
 QY 4321 ATGCAAAATCTGCCAAGTTGATTTCACTGTGGAACAACATGGAATTTATCTGAGCCTC 4380
 Db 4321 ATGCAAAATCTGCCAAGTTGATTTCACTGTGGAACAACATGGAATTTATCTGAGCCTC 4380
 QY 4381 GCGCCATTGGGACCCGTTACTCACCCGCTCCCTGTAATTTGTGTTATCAATTAACCG 4440
 Db 4381 GCGCCATTGGGACCCGTTACTCACCCGCTCCCTGTAATTTGTGTTATCAATTAACCG 4440
 QY 4441 GTTAATTCGTGCAATTGAACTTTGGTCTCATGTCTTATATCTTATCTGTCACCAATA 4500
 Db 4441 GTTAATTCGTGCAATTGAACTTTGGTCTCATGTCTTATATCTTATCTGTCACCAATA 4500
 QY 4501 GCAACCGGTTACATTAATCTGTTAGTGGCTTCGGAATACCCCTAGATGAGATT 4560
 Db 4501 GCAACCGGTTACATTAATCTGTTAGTGGCTTCGGAATACCCCTAGATGAGATT 4560
 QY 4561 GCCCACTCCCTTATGGGCGCTCGCTCGGTGGGGCCGAGAGAGAGCTCTGCGG 4620
 Db 4561 GCCCACTCCCTTATGGGCGCTCGCTCGGTGGGGCCGAGAGAGAGCTCTGCGG 4620
 QY 4621 TCTCGGAGCTTTGTGTCGAGGCCCCCAGCCAGAGAGGAGCGCATAGAGAGTGGG 4680
 Db 4621 TCTCGGAGCTTTGTGTCGAGGCCCCCAGCCAGAGAGGAGCGCATAGAGAGTGGG 4680
 QY 4681 CAA 4683
 Db 4681 CAA 4683

RESULT 4
 AAD00772
 ID AAD00772 standard; DNA; 4718 BP.
 XX
 AC AAD00772;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Adeno-associated virus serotype 1 DNA.
 XX
 KW Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
 KW cap protein; recombinant viral vector; gene delivery; gene therapy;
 KW vaccine; transgene; ss.
 XX
 OS Adeno associated virus serotype 1.
 XX
 FH Key
 FT repeat_unit
 FT 1..143
 FT /tag= a
 FT /label= 5'_ITR
 FT /note= "Inverted terminal repeat which is capable of
 FT forming T-shaped hairpin structure"
 FT 89..110
 FT /tag= b
 FT /bound_moiety= "Rep protein"
 FT 124..125
 FT /tag= c
 FT /note= "Terminal resolute site (TRS)"
 FT 219..226
 FT /tag= d
 FT /bound_moiety= "USP"
 FT /note= "E box"
 FT 236..299
 FT /tag= e
 FT /label= p5_promoter
 FT 237..245
 FT /tag= f
 FT /bound_moiety= "YY1 factor"
 FT 270..275
 FT /tag= g
 FT /label= p5_TATA-Box
 FT 299..306
 FT /tag= h
 FT /note= "YY1/p5 RNA"
 FT 335..2272
 FT /tag= j
 FT /product= "Rep 68"
 FT /function= "regulates replication and integration of AAV
 FT DNA into host cell's chromosome"
 FT /note= "The coding region is interrupted by intron"
 FT 335..2206
 FT /tag= i
 FT /product= "Rep 78"
 FT /function= "regulates replication and integration of AAV
 FT DNA into host cell's chromosome"
 FT 857..862
 FT /tag= 1
 FT /label= p19_TATA_Box
 FT 882..883
 FT /tag= m
 FT /note= "p19 RNA"
 FT 1007..2272
 FT /tag= o
 FT /product= "Rep 40"
 FT /function= "regulates replication and integration of AAV
 FT DNA into host cell's chromosome"
 FT /note= "The coding region is interrupted by intron"
 FT 1007..2206
 FT /tag= n
 FT /product= "Rep 52"
 FT /function= "regulates replication and integration of AAV
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 CDS
 FT
 CDS
 FT
 CDS
 FT

FT	DNA into host cell's chromosome"
FT	TATA_signal
FT	/tag= .1841
FT	/label= P40_TATA-BOX
FT	misc_feature
FT	/tag= .1876
FT	/note= "P40 RNA"
FT	intron
FT	/tag= k
FT	/note= "This region interrupts the coding sequence of Rep
FT	CDS
FT	/tag= r
FT	/product= "VP1 protein"
FT	/note= "Capsid protein"
FT	CDS
FT	/tag= s
FT	/product= "VP2 protein"
FT	/note= "Capsid protein"
FT	partial
FT	CDS
FT	/tag= t
FT	/product= "VP3 protein"
FT	/note= "Capsid protein"
FT	polyA_signal
FT	repeat_unit
FT	/tag= u
FT	/tag= v
FT	/label= 3' ITIR
FT	/note= "Inverted terminal repeat which is capable of
FT	forming T-shaped hairpin structure"
XX	
PN	WO20028061-A2.
PD	18-MAY-2000.
PF	02-NOV-1999; 99WO-US025694.
PR	05-NOV-1998; 98US-0107114P.
PA	(TYPE-) UNIV PENNSYLVANIA.
PI	wilson JM, Xiao W;
DR	WPI; 2000-376571/32.
DR	P-FSDB: AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
DR	AAY71169.
XX	
PT	Novel adeno-associated virus serotype 1 polynucleotide useful for
PT	preparation of medicament for delivery of a transgene to a host.
PS	Claim 1; Fig 1; 108pp; English.
XX	
CC	The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA
CC	characterised by two inverted terminal repeats (ITR) and open reading
CC	frames for rep and capsid (cap) proteins. The rep reading frame encodes
CC	four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading
CC	frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1
CC	sequence or its fragments particularly ITRs, rep and cap coding regions,
CC	are useful in production of recombinant viral vectors for gene delivery.
CC	These vectors can be used as gene therapy vectors, vaccine vectors or
CC	antisense delivery vectors. The AAV-1 does not induce the formation of
CC	neutralising antibodies specific to any serotype of AAV hence is useful
CC	for transforming host cells, and in the preparation of a medicament for
CC	the delivery of transgene to a host
XX	
SQ	Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
Query Match	90.8%; Score 4253.2; DB 3; Length 4718;
Best Local Similarity	94.7%; Pred No. 0;
Matches 4471; Conservative	0; Mismatches 208; Indels 43; Gaps 5

Db 1 TTGCCCATCTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGCTTCGCGACCAAGAGTCCGC 60

Qy 61 CGACGCCCGGGCTTTGGCCCGGGCGGCTCTAGTGAAGCAGCGAGCGCAGAGGAGT 120

Db 61 AGACGCGAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGGCGCGCAGAGGAGT 120

Qy 121 GCCAATCTCATCTAGTGGGT-----TCTGAGGGGTGGAGTCTGTA 163

Db 121 GGCAACTCATCTAGTGGGTAAATCGCAAGCGCTCCACGCTGCCGCTGACGCTGTA 180

Qy 124 CGTGAATTAGCTCATAGGTTAAGGAGGCTCTGTAATTAGAGTCAAGTGAAGTGTG- TTTTGC 222

Db 181 GGTAAATTAGCTCATAGG---GAGTGGCTCTGTAATTAGCTGTACAGTGAAGTCTTTTGC 237

Qy 223 GACATTTTGCACACCAATGTGTATACGCTGGTATTTTAAAGCCGAGTGAAGCACGAGGT 282

Db 228 GACATTTTGCACACCAAGTGTGCCATTTAAGGTATATATGGCCGAGTGAAGACAGAT 297

Qy 283 CTCCATTTTGAAGCGGAGGTTTGAACGCGACGCCCATGCGGGGTTTACAGATTTG 342

Db 298 CTCCATTTTGAACCGGAAATTTGAACGACGACGACCATGCGGGCTTTACAGATTCGT 357

Qy 343 GATTAAAGTCCCGACGCACTTGAACGACATCTGACCCGCACTTCTGACAGCTTGTGA 402

Db 358 GATCAAGGTGCGAGCGCACTGACAGACACTTCGCGGCAATTTCTGATCTGTTTGAAG 417

Qy 403 CTGGGTGCGCAGAGAAGATGGAGTTGCCGCAGATTTGACATGATCTGAATCTGAT 462

Db 418 CTGGGTGCGCAGAGAAGATGGAGTGTGCCCGGATTTCTGACATGATCTGAATCTGAT 477

Qy 463 TGAGCAGGCACTCTGACCGTGGCCGAGACCTGACAGCGCATTTCTGTCCACTGGCG 522

Db 478 TGAGCAGGCACTCTGACCGTGGCCGAGACCTGACAGCGCATTTCTGTGTCCATGGCG 537

Qy 523 CCGGTGATGTAAGGCCCGGAGGCCCTTTCTTGTTCAGTTGAGAAAGGCGAGTCTTA 582

Db 538 CCGGTGATGTAAGGCCCGGAGGCCCTTTCTTGTTCAGTTGAGAAAGGCGAGTCTTA 597

Qy 583 CTTCACACTCATATTTCTGTGAGAGACACGAGGGGTCAAAATCCATGTGCTGGAGCGCTT 642

Db 598 CTTCACACTCATATTTCTGTGAGAGACACGAGGGGTCAAAATCCATGTGCTGGAGCGCTT 657

Qy 643 CTTGATGTAATTAGCGACAAGCTGTGTGACAGCATCTACCGCGGATTCGAGCGGACCT 702

Db 658 CTTGATGTAATTAGCGACAAGCTGTGTGACAGCATCTACCGCGGATTCGAGCGGACCT 717

Qy 703 GCCCACTGTGTTCCGGTGAACCAAGACGCGTAATAGGCGCGAGAGGGGGAACAAAGTGT 762

Db 718 GCCCACTGTGTTCCGGTGAACCAAGACGCGTAATAGGCGCGAGAGGGGGAACAAAGTGT 777

Qy 763 GACAGAGTGTATATCCCCCACTACCTCTGCTCCCAAGACTGAGCCGAGCTGAGTGGC 822

Db 778 GAGAGAGTGTATATCCCCCACTACCTCTGCTCCCAAGACTGAGCTGAGTGGC 837

Qy 823 GTGAATTAACATGAGAGATATATAGCGGTGTTTAACTGTGCGCAAGCGCAACGAGCT 882

Db 838 GTGAATTAACATGAGAGATATATAGCGGTGTTTAACTGTGCGCAAGCGCAACGAGCT 897

Qy 883 CGTGGCGACAGCTCTGACCCACGTCAGCGACACCCAGAGAGGAAACAAAGAGATCTGAA 942

Db 898 CGTGGCGACAGCTCTGACCCACGTCAGCGACACCCAGAGAGGAAACAAAGAGATCTGAA 957

Qy 943 CCCCATACTGACGCGGCTGTCAATCCGGTCAAAAACCTCCGACAGCTATCAATGAGTGGT 1002

Db 958 CCCCATACTGACGCGGCTGTCAATCCGGTCAAAAACCTCCGAGGCTATCAATGAGTGGT 1017

Qy 1003 CGGTGTGCTGTGAGACCGGGGCACTACCTCCGAGAGCAGTGAATCCAGAGGACCAAGC 1062

Db 1018 CGGTGTGCTGTGAGACCGGGGCACTACCTCCGAGAGCAGTGAATCCAGAGGACCAAGC 1077

Qy 1063 CTCGTACATCTCTTCAACGCGGCTCCCACTCGCGGTCCAGATCAAGGCTCGCTCTGGA 1122

Db	1078	CTCGATACATCTCTTCAACGCCGCTTCCAACTCGCGGTCCAGATCAAGGCCGCTCTGGA	1137
Qy	1123	CAATGCGGCAAGATCATGCGCTGACCAAAATCCCGCCCGCATCTACCTGTATGGCCCGC	1182
Db	1138	CAATGCGGCAAGATCATGCGCTGACCAAAATCCCGCCCGCATCTACCTGTATGGCCCGC	1197
Qy	1183	TCGCGCCGCGACATTTAAACCAACCGCATTTTACCGCATCTGTAGACTGAACGCGTACGA	1242
Db	1198	TCGCGCCGCGACATTTAAACCAACCGCATCTGTAGACTGAACGCGTACGA	1257
Qy	1243	CCCTGCTACGCGCGCTCCGCTCTTTCTCGGCTGCGGCCCAAGAAAGTTTCGAAAACGCA	1302
Db	1258	ACCTGCTACGCGCGCTCCGCTCTTTCTCGGCTGCGGCCCAAGAAAGTTTCGAAAACGCA	1317
Qy	1303	CACATCTGCGCTTTTGGCGCGGACCAACGCGGCAAGACCAACATCTGCGGAAGCATGCG	1362
Db	1318	CACATCTGCGCTTTTGGCGCGGACCAACGCGGCAAGACCAACATCTGCGGAAGCATGCG	1377
Qy	1363	CCAGCGCGTGCCTTCTACGCGCTGCTCAACTGACACATGAGAACTTTCCCTTCAACGA	1422
Db	1378	CCAGCGCGTGCCTTCTACGCGCTGCTCAACTGACACATGAGAACTTTCCCTTCAATGA	1437
Qy	1423	TTGCGTGCACAAAGATGTGATCTGCTGGAAGAGGCAAGATGACGCGCAAGGTGTGGA	1482
Db	1438	TTGCGTGCACAAAGATGTGATCTGCTGGAAGAGGCAAGATGACGCGCAAGGTGTGGA	1497
Qy	1483	GTCCGCGCAAGGCCATTTCTCGCGCGGACGAAGGTGCGTGAACCAAAAGTGCAGTCTGC	1542
Db	1498	GTCCGCGCAAGGCCATTTCTCGCGCGGACGAAGGTGCGTGAACCAAAAGTGCAGTCTGC	1557
Qy	1543	CGCCAGATCGATCCCAACCCCGGTGATGCTCACTCCAAACCAACATGTGCGCGTAT	1602
Db	1558	CGCCAGATCGATCCCAACCCCGGTGATGCTCACTCCAAACCAACATGTGCGCGTAT	1617
Qy	1603	TGACGGGAACGACCACTTTCAGACACAGACCGCTTGACAGACCGGATGTTCAAAAT	1662
Db	1618	TGACGGGAACGACCACTTTCAGACACAGACCGCTTGACAGACCGGATGTTCAAAAT	1677
Qy	1663	TGAATCAACCCCGCTGTGAGCATGACTTTGGCAAGTGAACAAAGCAGAAATCAAAAG	1722
Db	1678	TGAATCAACCCCGCTGTGAGCATGACTTTGGCAAGTGAACAAAGCAGAAATCAAAAG	1737
Qy	1723	GTTCCTCGCTGCGCGCAGATCAAGTGAACGAGGTGCGCATGATTTCTACGTCAGAAA	1782
Db	1738	GTTCCTCGCTGCGCGCAGATCAAGTGAACGAGGTGCGCATGATTTCTACGTCAGAAA	1797
Qy	1783	GGGTGAGCCAAACAGACCCCGCCGATGACGCGGATAAAGCGAACCCAAACGCGGC	1842
Db	1798	GGGTGAGCCAAACAGACCCCGCCGATGACGCGGATAAAGCGAACCCAAACGCGGC	1857
Qy	1843	CTGCGCCCTCAGTCCCGGATTCATGAGCTCAGACGCGGAAGAGCTCCGCTGAGACTTTGC	1902
Db	1858	CTGCGCCCTCAGTCCCGGATTCATGAGCTCAGACGCGGAAGAGCTCCGCTGAGACTTTGC	1917
Qy	1903	CGACAGGTACCAAAACAAATGTTCTGTCAGCGCGGACATGCTTCAAGATGCTTTCCCTG	1962
Db	1918	CGACAGGTACCAAAACAAATGTTCTGTCAGCGCGGACATGCTTCAAGATGCTTTCCCTG	1977
Qy	1963	CAAAACATGCGAGAAATGAATCAGAAATTTCAACATTTGCTTCAACGCAACGGAACAGAGA	2022
Db	1978	CAAAACATGCGAGAAATGAATCAGAAATTTCAACATTTGCTTCAACGCAACGGAACAGAGA	2037
Qy	2023	CTGTTCAGAAATGTTTCCCGCGCTGTGAGAAATCTCAACCGGCTGTCAGAAAGAGAGCTA	2082
Db	2038	CTGTTCAGAAATGTTTCCCGCGCTGTGAGAAATCTCAACCGGCTGTCAGAAAGAGAGCTA	2097
Qy	2083	TCGGAACCTCTGTCCCATTCATCATCTGCTGGGCGGGCTCCGAGATTTGCTTGCCTGCGC	2142
Db	2098	TCGGAACCTCTGTCCCATTCATCATCTGCTGGGCGGGCTCCGAGATTTGCTTGCCTGCGC	2157
Qy	2143	CTGCGATCTGGTCAACGTGATCTGAGTGAATGATGATGATGATGATGATGATGATGATGATG	2202
Db	2158	CTGCGATCTGGTCAACGTGATCTGAGTGAATGATGATGATGATGATGATGATGATGATGATG	2217

Qy	2203	CAGGATGCGTGGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACTCTGTAGGGCA	2262
Db	2218	CAGGATGCGTGGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACTCTGTAGGGCA	2277
Qy	2263	TTCCGACATGCTGGGACTTTGAAACCTGAGCCCGGAAACCAAGCCCAACGCAAAAGC	2322
Db	2278	TTCCGACATGCTGGGACTTTGAAACCTGAGCCCGGAAACCAAGCCCAACGCAAAAGC	2337
Qy	2323	AGACGACGCGCGGGGTCTGCTGCTTCTGCTCAAGTACCTGAGACCTTTCAACGAC	2382
Db	2338	AGACGACGCGCGGGGTCTGCTGCTTCTGCTCAAGTACCTGAGACCTTTCAACGAC	2397
Qy	2383	TCGACAGGGGGAGCCCTCAACCGCGGATGACGCGCCCTGAGACGACAAAGGCT	2442
Db	2398	TCGACAGGGGGAGCCCTCAACCGCGGATGACGCGCCCTGAGACGACAAAGGCT	2457
Qy	2443	ACGACACGACCTCAAGCGGGTGAATCCGTAACCTGCGGTATTAACACCGCGACGCG	2502
Db	2458	ACGACACGACCTCAAGCGGGTGAATCCGTAACCTGCGGTATTAACACCGCGACGCG	2517
Qy	2503	AGTTCAAGAGCGTCTGCAAGAAATGCTTTTGGGGCAACCTCGGCGACGACTT	2562
Db	2518	AGTTCAAGAGCGTCTGCAAGAAATGCTTTTGGGGCAACCTCGGCGACGACTT	2577
Qy	2563	TCGAGCCCAAGAGGTTCTGCAACCTTTTGGTCTGTGTGAGAAAGTGTCAAGACG	2622
Db	2578	TCGAGCCCAAGAGGTTCTGCAACCTTTTGGTCTGTGTGAGAAAGTGTCAAGACG	2637
Qy	2623	CTCTGGAAGAAAGTCCCGGTAGAGCGAGTGCACCAAGACCGACCTCTCGGCA	2682
Db	2638	CTCTGGAAGAAAGTCCCGGTAGAGCGAGTGCACCAAGACCGACCTCTCGGCA	2697
Qy	2683	TTGSCAAGACAGGCAAGCGCTGTAAGAAAGAGACTCAATTTTGTGAGCTGAGACT	2742
Db	2698	TTGSCAAGACAGGCAAGCGCTGTAAGAAAGAGACTCAATTTTGTGAGCTGAGACT	2757
Qy	2743	CAGAGTCACTCCCGACCCCAACACTCTCGAGAACTCCACGACAAACCCCGCTGCTG	2802
Db	2758	CAGAGTCACTCCCGACCCCAACACTCTCGAGAACTCCACGACAAACCCCGCTGCTG	2817
Qy	2803	GACCTACATCAATGCTTACAGCGCGGTGCGCAACCAATGSCAGAAATTAACGAAGCGCG	2862
Db	2818	GACCTACATCAATGCTTACAGCGCGGTGCGCAACCAATGSCAGAAATTAACGAAGCGCG	2877
Qy	2863	ACGAGTGGGTATGCTTCAAGAAATTTGGCAATTCAGATGCTGGCGACAGAG	2922
Db	2878	ACGAGTGGGTATGCTTCAAGAAATTTGGCAATTCAGATGCTGGCGACAGAG	2937
Qy	2923	TCATCACACCAAGACACCCGAACATGGGCTTTGCCACTTATTAACAACCACTCTACAGC	2982
Db	2938	TCATCACACCAAGACACCCGAACATGGGCTTTGCCACTTATTAACAACCACTCTACAGC	2997
Qy	2983	AAATCTCAGTGTCTCAACGGGGGCGACGAACGACCACTACTTTCGAGTACGACACC	3042
Db	2998	AAATCTCAGTGTCTCAACGGGGGCGACGAACGACCACTACTTTCGAGTACGACACC	3057
Qy	3043	CTTGGGGGTATTTTGAATTTCAACAGATTCATGCAATTTCTCAACAGTACGAGC	3102
Db	3058	CTTGGGGGTATTTTGAATTTCAACAGATTCATGCAATTTCTCAACAGTACGAGC	3117
Qy	3103	GACTCATCAACAAATTTGGGAGATTCGCGCCCAAGAGACTCACTTCAAGCTTTCAACA	3162
Db	3118	GACTCATCAACAAATTTGGGAGATTCGCGCCCAAGAGACTCACTTCAAGCTTTCAACA	3177
Qy	3163	TCCAAGTCAAGAGAGTCAACGAAATGATGCGGTCAAGCAATGCTTAATTAACCTTAACA	3222
Db	3178	TCCAAGTCAAGAGAGTCAACGAAATGATGCGGTCAAGCAATGCTTAATTAACCTTAACA	3237
Qy	3223	GCAAGGTTCAAGTCTTGTGAGCTCGAGTGAACAGTTCCCGTACGTCCTGCGCTTGC	3282
Db	3238	GCAAGGTTCAAGTCTTGTGAGCTCGAGTGAACAGTTCCCGTACGTCCTGCGCTTGC	3297

QY 3283 ACCAGGGGCTGCTCCCTCCGTTCCGGGCGAGCGNTTCAATGATTCGCGAGTAAAGGCTACC 3342
 DB 3298 ACCAGGGGCTGCTCCCTCCGTTCCGGGCGAGCGNTTCAATGATTCGCGAGTAAAGGCTACC 3357
 QY 3343 TAAAGCTCAACAATGGAGCGAGCGAGTGGAGCGCTCATCTTTTACCTGCTGGAAATATTT 3402
 DB 3358 TGAAGCTCAACAATGGAGCGAGCGAGTGGAGCGCTCATCTTTTACCTGCTGGAAATATTT 3417
 QY 3403 TCCCATGCGAGATGCTGAGAAAGGGCAATTAATCTTACCTTACGCTACCACTTTCAGAGACG 3462
 DB 3418 TCCCTTCTCAGATGCTGAGAAAGGGCAACAATTTACCTTACGCTACCACTTTCAGAGAG 3477
 QY 3463 TGACCTTCCACAGAGCTAGCGAGCGAGCGAGCTGGACCGGCTGATGATCTCTCA 3522
 DB 3478 TGCTTTTCCACAGAGCTAGCGAGCGAGCGAGCTGGACCGGCTGATGATCTCTCTCA 3537
 QY 3523 TCGACAGTACCTGTATTAATCTGAAACAGAACTCAAACTCACTGATCCGGAAGTCCCAAAACA 3582
 DB 3538 TCGACAAATACCTGTATTAATCTGAAACAGAACTCAAAATCAAGTCGGAAAGTCCCAAAACA 3597
 QY 3583 AGGACTTGTCTTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTCAGTCCCAAAATCTGGC 3642
 DB 3598 AGGACTTGTCTTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTCAGTCCCAAAATCTGGC 3657
 QY 3643 TACCTGAGACCTGTATTAATCCGGAGCGAGCGGCTTTTAAACAAAAACAGAAACAACA 3702
 DB 3658 TACCTGAGACCTGTATTAATCCGGAGCGAGCGGCTTTTAAACAAAAACAGAAACAACA 3717
 QY 3703 GCAACTTTACCTGAGCTGTGCTTCAAAATTAATTAATGAGCGGTGAATCTTAATCA 3762
 DB 3718 GCAATTTTACCTGAGCTGTGCTTCAAAATTAATTAATGAGCGGTGAATCTTAATCA 3777
 QY 3763 ACCCTGGGACCTGCTATGAGCCCTCAACAAGACGAAAGCAAAATTTCTTCCCATGAGCG 3822
 DB 3778 ACCCTGGGACCTGCTATGAGCCCTCAACAAGACGAAAGCAAAATTTCTTCCCATGAGCG 3837
 QY 3823 GTGTCAATGATTTTGGAAAGAGCGCGGAGCTTCAACACATGCAATTTGGACAATGCA 3882
 DB 3838 GTGTCAATGATTTTGGAAAGAGCGCGGAGCTTCAACACATGCAATTTGGACAATGCA 3897
 QY 3883 TGATCAGACGAAAGAGAAATCAAAAGCACTAAACCCCGTGGCAACCGAAAGATTTGGGA 3942
 DB 3898 TGATTAACAGACGAAAGAGAAATTAAGCACTAAACCCCGTGGCAACCGAAAGATTTGGGA 3957
 QY 3943 CTGTGGAGCTAATCTCCAGAGCAGCAGACAGACCCCTGCGACCGGAGATTTGCATGTA 4002
 DB 3958 CCGTGGAGCTAATTTCCAGAGCAGCAGACAGACCCCTGCGACCGGAGATTTGCATGTA 4017
 QY 4003 TGGAGAGCTTACCTGGAATGCTGTGGCAAGACAGAGATTAATCTGCAAGGCTCTAATTT 4062
 DB 4018 TGGAGAGCTTACCTGGAATGCTGTGGCAAGATTAAGAGCTTAATCTGCAAGGCTCTAATTT 4077
 QY 4063 GGGGCAAAATTTCTCAACGAGTGGACAATTTCAACCCGCTCTCTCAATGGGCGGCTTTG 4122
 DB 4078 GGGGCAAAATTTCTCAACGAGTGGACAATTTCAACCCGCTCTCTCAATGGGCGGCTTTG 4137
 QY 4123 GACTTAAGCACCCGCTCTCTAGATCTTCAATCAAAACAGCCGCTTCTCTGCGAATCTCTC 4182
 DB 4138 GACTCAAGAACCCGCTCTCTAGATCTTCAATCAAAACAGCCGCTTCTCTGCGAATCTCTC 4197
 QY 4183 CGGAGAGTTTTGCGCTACAAAGTTTGCTTCAATCATCAACCAATATTTCCACAGACAG 4242
 DB 4198 CGGAGAGTTTTGCGCTACAAAGTTTGCTTCAATCATCAACCAATATTTCCACAGACAG 4257
 QY 4243 TGAGCGTGGAGATTTGAGAGCTGCAAGAAAGAAACAGCAAAAGCTGGAATCCGAG 4302
 DB 4258 TGAATGTGGAATTTGAATGGAGCTGCAAGAAAGAAACAGCAAAAGCTGGAATCCGAG 4317
 QY 4303 TGGAGTATACATTAATGATGCAAAATGTCACAGTTGATTTTACCTGTGAGCAACAATG 4362
 DB 4318 TGGAGTATACATTAATGATGCAAAATGTCACAGTTGATTTTACCTGTGAGCAACAATG 4377
 QY 4363 GACTTTTACTAGAGCTTGGCCCATTTGGCACCCGTTACCTCAACCCGTTCCCTGTAAATGT 4422

DB 4378 GACTTTTACTAGAGCTCGGCCCATTTGGACCCGTTACCTTACCCGCTGTAAATTAAC 4437
 QY 4423 GTGTAAATCAATTAACCGGTTAATTTGCTGCAATTTGCTGCTCATGCTCTAATTA 4482
 DB 4438 GTGTAAATCAATTAACCGGTTGATTTGCTGCAATTTGCTGCTCATGCTCTAATTA 4497
 QY 4483 TCTTATCTGTGCAATAGCAACCGGTTACATTAATGCTAGTTGAGCTTGGCA-- 4540
 DB 4498 TCTTATC-GGTTACCATGTTAATGCTTACATTTAATCTGTTGAGCTTGGCAATA 4556
 QY 4541 -----ATACCCCTAGTATGATGAGTTGCCACATCCTCTATGCGCGC 4581
 DB 4557 AAGACTTACGTCATGCGGTTACCCCTAGTATGAGTTGCCACATCCTCTGCGCGC 4616
 QY 4582 TCGCTGCTGCTGTGGGGCGGCGAGACAGAGCTCTGCTGCTGCGACCTTTGCTCGCA 4641
 DB 4617 TCGCTGCTGCTGTGGGGCGGCGAGACCAAGGTCGCAAGCGGCAAGCTCTGCTGCC 4676
 QY 4642 GGGCCCAACGAGGAGCGGCGCATPAGAGGAGTGGCCAA 4683
 DB 4677 GGCCCAACGAGGAGCGGCGCATPAGAGGAGTGGCCAA 4718

 RESULT 5
 ADE76507
 ID ADE76507 standard; DNA: 4718 BP.
 AC ADE76507;
 DT 29-JAN-2004 (first entry)
 XX
 DE Adeno-associated virus (AAV) related DNA, SEQ ID No 6.
 XX
 KM adeno-associated virus; AAV, cytosolic; antiposratic; antirheumatic;
 KM antidiabetic; neuroprotective; antidiabetic; antihypertensive;
 KM dermatological; antineoplastic; gene therapy; vaccine;
 KM hyperlipidemic; cancer; psoriasis; autoimmune disease;
 KM rheumatoid arthritis; multiple sclerosis; diabetes;
 KM autoimmune thyroiditis; scleroderma; Crohn's disease; gene; de.
 OS Adeno-associated virus 1.
 XX
 EN BP1310571-A2.
 XX
 PD 14-MAY-2003.
 XX
 PF 12-NOV-2002; 2002EP-00257826.
 XX
 PR 13-NOV-2001; 2001US-0350607P.
 PR 17-DEC-2001; 2001US-0341117P.
 PR 01-MAY-2002; 2002US-0377066P.
 PR 05-JUN-2002; 2002US-0386675P.
 XX
 PA (UPE-) UNIV PENNSYLVANIA.
 XX
 PI Gao G, Wilson JM, Alvira M;
 DR WPI; 2003-450984/43.
 XX
 PT Detecting adeno-associated virus sequences in a sample, useful for e.g.
 PT preventing or treating hyperlipidemic or autoimmune diseases,
 PT comprising subjecting a sample having a DNA to amplification via
 PT polymerase chain reaction.
 XX
 PS Claim 14; SEQ ID NO 6; 419pp; English.
 XX
 CC The invention relates to a novel method for detecting adeno-associated
 CC virus (AAV) sequences in a sample, which comprises subjecting a sample
 CC containing a DNA to amplification via a polymerase chain reaction (PCR).
 CC The AAV sequence have the following activities: cytosolic,
 CC antiposratic, antirheumatic, antidiabetic, neuroprotective,
 CC antidiabetic, antihypertensive, dermatological, and antineoplastic. The AAV

CC sequence can be used in gene therapy or as part of a vaccine to treat
CC disorders. The method is useful in detecting and/or identifying AAV
CC sequences and isolating novel sequences that are identified. The
CC sequences may be used e.g. for preventing or treating hyperproliferative
CC conditions such as cancers and psoriasis, and other autoimmune diseases
CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
CC chondritis, scleroderma or Crohn's disease. This polynucleotide sequence
CC represents an AAV related DNA sequence of the invention.
XX

SQ Sequence 4718 BP, 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 10; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;

Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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QY 1 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGGCGCAAAAGTCCG 60
Db 1 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGGCGCAAAAGTCCG 60
QY 61 CGAGCGCGGCGCTTGGCGCGCGCTCAGTGAAGCGAGCGCGCGAGAGGAGTG 120
Db 61 AGACGCGCAGAGCTCTGCTCTGCGGCGCCACCGAGCGAGCGCGAGAGGAGTG 120
QY 121 GCCAATCTCATCTACAGGCGGT-----TCCGAGAGGCGTGAAGTCTGA 163
Db 121 GCGAATCTCATCTACAGGCGGTATGCGAGCGCGCTCCACGCGTCCCGTCAAGCTGA 180
QY 164 CGTGAATTAAGTCAATAGGCTTGAAGAGTCTCTGTAATGAAGTCACTGAGTG-TTTTGC 222
Db 181 CGTAAATTAAGTCAATAGG---GAGTGTCTCTGTAATGAGTCTGAGAGGCTTTTGC 237
QY 223 GACATTTTGGCAACCATGAGTGTCAAGCGGTATTAAGCCGAGTGAAGCAGAGGAGT 282
Db 238 GACATTTTGGCAACCATGAGTGTCAAGCGGTATTAAGCGGTGAAGCAGAGGAGT 297
QY 283 CTCATTTTGAAGCGGAGGTTTGAACGCGAGCGCATGCGGCGGTTTGAAGATTTG 342
Db 298 CTCATTTTGAACGCGGAAATTTGAACGAGCAGCAGCATGCGGCGCTTCAAGATGCT 357
QY 343 GATTAAAGTCCCGACGAGCTTTGACGAGCATCTGCGCGCATTTTCTGACAGCTTTGAA 402
Db 358 GATCAAGGTGCGGAGCGACCTGAGCAGACCATCTGCGGCGATTTCTGACTGTTTGTAG 417
QY 403 CTGAGTGGCGGAGAGGATGGAGTTGCGCGAGATCTGACATGAGTCTGAATCTGAT 462
Db 418 CTGAGTGGCGGAGAGGATGGAGTTGCGCGAGATCTGACATGAGTCTGAATCTGAT 477
QY 463 TGACGAGGCAACCCCTGACCGTGGCGAGAGCTGACGCGCATCTCTGCTCACTGGCG 522
Db 478 TGACGAGGCAACCCCTGACCGTGGCGGAGAGCTGACGCGCATCTCTGCTCAATGGCG 537
QY 523 CCGCGTGAATAGGCGCGGAGCGCTCTTCTTTGTTCAATTGGAAGGCGAGTCTTA 582
Db 538 CCGCGTGAATAGGCGCGGAGCGCTCTTCTTTGTTCAATTGGAAGGCGAGTCTTA 597
QY 583 CTTCACCTTCATATTTCTGAGTGAAGCAACGCGGCGTCAATCAATGCTGCGCGCTT 642
Db 598 CTTCACCTTCATATTTCTGAGTGAAGCAACGCGGCGTCAATCAATGCTGCGCGCTT 657
QY 643 CTTGAGTCAAGTTAGCAGCAAGCTGTGACAGCATCTACCGCGGATCGAGCGACCT 702
Db 658 CTTGAGTCAAGTTAGGAGCAAGCTGTGACAGCATCTACCGCGGATCGAGCGACCT 717
QY 703 GCCCAACTGTTGCGCGGTGACCAAGACGCTGAATGCGCGCGAGAGGAGGAACTAGTGT 762
Db 718 GCCCAACTGTTGCGCGGTGACCAAGACGCTGAATGCGCGCGAGAGGAGGAACTAGTGT 777
QY 763 GAGCAGAGTCACTATCCCACTACTCTGCGCAAGCTAGCGCGGAGCTGAGTGGCG 822
Db 778 GAGCAGAGTCACTATCCCACTACTCTGCGCAAGCTAGCGCGGAGCTGAGTGGCG 837
QY 823 GTGACATAACATGAGAGATATATAGCGCGTGTTTAAACTGCGCGAGCGCAACGCGCT 882
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Db 838 GTGACATAACATGAGAGATATATAGCGCGCTGTTTGAACCTGCGCGAGCGCAACGCGCT 897
QY 883 GTGCGCGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 942
Db 898 GTGCGCGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 957
QY 943 CCCCAATCTGAGCGCGCTGATCCCGGTCAAAAACCTCCGCAAGCTTCAATGAGCTGCT 1002
Db 958 CCCCAATCTGAGCGCGCTGATCCCGGTCAAAAACCTCCGCGCTTCAATGAGCTGCT 1017
QY 1003 CGGAGTGTGAGACCGGCGCATCACTCCGAGAGCAGTGAATCCAGAGGACCAAGC 1062
Db 1018 CGGAGTGTGAGACCGGCGCATCACTCCGAGAGCAGTGAATCCAGAGGACCAAGC 1077
QY 1063 CTCTGATCTCTCTTCAACGCGCGCTCCAATCTCGCGTCCCAATCAAGCGCGCTTGA 1122
Db 1078 CTCTGATCTCTCTTCAACGCGCGCTCCAATCTCGCGTCCCAATCAAGCGCGCTTGA 1137
QY 1123 CAATGCGCGCAAGATCAATGCGGCTGACCAATCCGCGCGGACCTAATCTGTAAGCGCGCG 1182
Db 1138 CAATGCGCGCAAGATCAATGCGGCTGACCAATCCGCGCGGACCTAATCTGTAAGCGCGCG 1197
QY 1183 TCCGCGCGCGACATTAACCAACCGCATTTACCGCATCTTGAAGCTGAACGCGTACGA 1242
Db 1198 TCCGCGCGCGACATTAACCAACCGCATTTACCGCATCTTGAAGCTGAACGCGTACGA 1257
QY 1243 CCTGCTTACGCGCGCTCGTCTTTCTCGGCTGGGCGCCAGAAAAGTTTGGAAAACGCA 1302
Db 1258 ACTGCTTACGCGCGCTCGTCTTTCTCGGCTGGGCGCCAGAAAAGTTTGGGAAACGCA 1317
QY 1303 CACCATCTGCTGTTTGGGCGCGGACCAACGCGGAGCAACATCCGCGGAAAGCATGCG 1362
Db 1318 CACCATCTGCTGTTTGGGCGCGGACCAACGCGGAGCAACATCCGCGGAAAGCATGCG 1377
QY 1363 CCACGCGCTGCTTCTTCAACGCTGCTCACTGACCAATGAGAACTTCCCTTCAACGA 1422
Db 1378 CCACGCGCTGCTTCTTCAACGCTGCTGCTCACTGACCAATGAGAACTTCCCTTCAATGA 1437
QY 1423 TTGCGTGAACAAGTGTGATCTGTGAGAGAGGCGCAAGTGAACGCGCATAGTGTGGA 1482
Db 1438 TTGCGTGAACAAGTGTGATCTGTGAGAGAGGCGCAAGTGAACGCGCATAGTGTGGA 1497
QY 1483 GTCCGCAAGGCGATTTCCGCGCGGACCAAGGTGCGGTGAGCAAAAAGTCAAGTGTGTC 1542
Db 1498 GTCCGCAAGGCGATTTCCGCGCGGACCAAGGTGCGGTGAGCAAAAAGTCAAGTGTGTC 1557
QY 1543 CGCCCAATCGATCCCAACCCCGGTGATGCTACCTCCCAACCAATGTCGCGCGTAT 1602
Db 1558 CGCCCAATCGATCCCAACCCCGGTGATGCTACCTCCCAACCAATGTCGCGCGTAT 1617
QY 1603 TGACGAGAAACAGCACTTTCAGACACAGACGCGTTGAGAGACCGGATGTTCAATT 1662
Db 1618 TGACGAGAAACAGCACTTTCAGACACAGACGCGTTGAGAGACCGGATGTTCAATT 1677
QY 1663 TGAATCAACCGCGCTGAGAGTGAATCTTTGGAAGTGAACAAGAGAGAAAGTCAAGA 1722
Db 1678 TGAATCAACCGCGCTGAGAGTGAATCTTTGGAAGTGAACAAGAGAGAAAGTCAAGA 1737
QY 1723 GTTCTTCCGTGGCGGAGATCACTGACGAGTGAAGTGGCGCATGTTTACGTCAGAAA 1782
Db 1738 GTTCTTCCGTGGCGGAGATCACTGACGAGTGAAGTGGCGCATGTTTACGTCAGAAA 1797
QY 1783 GGGTGAAGCCAAACAAGACCCCGCGATGACGCGCGATTAAGAGAGAGCCCAAGCGGCG 1842
Db 1798 GGGTGAAGCCAAACAAGACCCCGCGATGACGCGCGATTAAGAGAGAGCCCAAGCGGCG 1857
QY 1843 CTGCGCTCAAGTGGCGGATCATGAGTCAAGCGCGGAAAGAGCTCGGATGAGCTTTGC 1902
Db 1858 CTGCGCTCAAGTGGCGGATCATGAGTCAAGCGCGGAAAGAGCTCGGATGAGCTTTGC 1917
QY 1903 CGACAGGTACCAAAAACAATGTTCTGTCACGCGGCGATCTTCAGATGCTGTTTCCCTG 1962
Db 1918 CGACAGGTACCAAAAACAATGTTCTGTCACGCGGCGATCTTCAGATGCTGTTTCCCTG 1977
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Qy	1963	CAAAACATGCGAGATGATCAGAAATTTCAACATTTGCTTCAACGACGGGACCAAGAGA	2022
Db	1978	CAAGACATGCGAGAGAAATGAAATCAGAAATTTCAACATTTGCTTCAACGACGGGACCAAGAGA	2037
Qy	2023	CTGTTCAGAAATGTTTTCCCGGCGGTGTCAGAAATCTTCAACCGGTCTCAGAAAAGAGACGTA	2082
Db	2038	CTGTTCAGAGAGTCTTCCCGGCGGTGTCAGAAATCTTCAACCGGTCTCAGAAAAGAGACGTA	2097
Qy	2083	TCGGAATCTGTGTCATTCATCTGTGGGGCGGGCTCCGAGATTTGCTTCTCGGC	2142
Db	2098	TCGGAATCTGTGTCATTCATCTGTGGGGCGGGCTCCGAGATTTGCTTCTCGGC	2157
Qy	2143	CTGCGATCTGTGTCACGTCGATCTGATGACTGTGTTCTGAGCAATTAATGACTTAAAC	2202
Db	2158	CTGCGATCTGTGTCACGTCGATCTGATGACTGTGTTCTGAGCAATTAATGACTTAAAC	2217
Qy	2203	CAGGTATGCTGCCGATGTTATCTTCCAGATTTGCTGAGAGCAAACTCTCTGAGGCA	2262
Db	2218	CAGGTATGCTGCCGATGTTATCTTCCAGATTTGCTGAGAGCAAACTCTCTGAGGCA	2277
Qy	2263	TTCCGCACTGTGTCAGTTGAACTTGAGAGCCCGGAAACCCAAAGCCAAACGAGAAAAGC	2322
Db	2278	TTCCGCACTGTGTCAGTTGAACTTGAGAGCCCGGAAACCCAAAGCCAAACGAGAAAAGC	2337
Qy	2323	AGGACGACGCGCGGGGTCTGTGCTTCTGTGCTACAAATGATCTGAGACCTTCAACGGAC	2382
Db	2338	AGGACGACGCGCGGGGTCTGTGCTTCTGTGCTACAAATGATCTGAGACCTTCAACGGAC	2397
Qy	2383	TCGACAAAGGGGAGCCGCTCAACGCGGCGAGTGCAGCGGCCCTCTGAGACGACAAAGCTT	2442
Db	2398	TCGACAAAGGGGAGCCGCTCAACGCGGCGAGTGCAGCGGCCCTCTGAGACGACAAAGCTT	2457
Qy	2443	ACGACCGACACTTAAAGCGGGTGAATCCGTACCTCGGCTATTAACAACGCCGACGCGC	2502
Db	2458	ACGACCGACACTTAAAGCGGGTGAATCCGTACCTCGGCTATTAACAACGCCGACGCGC	2517
Qy	2503	AGTTTCAGAGACGTCTGCAAAAGATACGCTTTTGGGGGCAACCTCGGCGAGACAGTCT	2562
Db	2518	AGTTTCAGAGACGTCTGCAAAAGATACGCTTTTGGGGGCAACCTCGGCGAGACAGTCT	2577
Qy	2563	TCGACGCGCAAGAGAGGGTCTTCAACCTTTTGTGTTGAGAGAGTCTTAAGACG	2622
Db	2578	TCGACGCGCAAGAGAGGGTCTTCAACCTTTTGTGTTGAGAGAGTCTTAAGACG	2637
Qy	2623	CTCCTGGAAGAAACGTCCGGTGAAGACGTGCGCAACAGACCGACCTCTCTCGGCGCA	2682
Db	2638	CTCCTGGAAGAAACGTCCGGTGAAGACGTGCGCAACAGACCGACCTCTCTCGGCGCA	2697
Qy	2683	TTGGCAAGACAGGCGCAGCGCCGCTAAAAAAGAGACTCAATTTTGTGTCAGACTGGCGACT	2742
Db	2698	TTGGCAAGACAGGCGCAGCGCCGCTAAAAAAGAGACTCAATTTTGTGTCAGACTGGCGACT	2757
Qy	2743	CAGAGTCAGTCCCGGACCCCAACACTCTCTGAGAACTCTCAGCAACCCCCCTGCTGTGG	2802
Db	2758	CAGAGTCAGTCCCGGATCCCAACACTCTCTGAGAACTCTCAGCAACCCCCCTGCTGTGG	2817
Qy	2803	GACCTACTACATAGGCTTCAAGCGGTGGCGCAACAAATGGCAGAACTTAAGAAAGCGCGC	2862
Db	2818	GACCTACTACATAGGCTTCAAGCGGTGGCGCAACAAATGGCAGAACTTAAGAAAGCGCGC	2877
Qy	2863	ACGAGTGGGTAAATGCTCAGGAAATTTGCAATTTGATTCACATGCTGGCGCACAGAG	2922
Db	2878	ACGAGTGGGTAAATGCTCAGGAAATTTGCAATTTGATTCACATGCTGGCGCACAGAG	2937
Qy	2923	TCATACCAACCAAGCAATGGGCTTTGGCCCACTTATTAACAACCACTCTTAACAAGC	2982
Db	2938	TCATACCAACCAAGCAATGGGCTTTGGCCCACTTATTAACAACCACTCTTAACAAGC	2997
Qy	2983	AAATCTCAAGTCTTCAACGGGGGCGACGACCAACCACTAATTGGGCTACAGCAACC	3042
Db	2998	AAATCTCAAGTCTTCAACGGGGGCGACGACCAACCACTAATTGGGCTACAGCAACC	3057

Qy	3043	CTGGGGGTATTTTGAATTTCAAGATTTCCACTGCCATTTCTGACACGATGCGAGC	3102
Db	3058	CTGGGGGTATTTTGAATTTCAAGATTTCCACTGCCATTTCTGACACGATGCGAGC	3117
Qy	3103	GACTCATCAACAAATTTGGGGATTTCCGGCTCCAAAGACTCAACTTAAGCTTTCAACA	3162
Db	3118	GACTCATCAACAAATTTGGGGATTTCCGGCTCCAAAGACTCAACTTAAGCTTTCAACA	3177
Qy	3163	TCGAATCAAGGAGGTCAACGACGATGAGCGCTCAACCACTGCTTAATACCTTACCA	3222
Db	3178	TCGAATCAAGGAGGTCAACGACGATGAGCGCTCAACCACTGCTTAATACCTTACCA	3237
Qy	3223	GCAAGGTTCAAGCTTTGTGGAATCTGAGATCCAGATTCGGTACGTCCTGCGCTTGGC	3282
Db	3238	GCAAGGTTCAAGCTTTGTGGAATCTGAGATCCAGATTCGGTACGTCCTGCGCTTGGC	3297
Qy	3283	ACCAAGGCTGCTCTCCCTCCGTTCCCGGCGACGTGTTCAATGATTCGGCACTACGGCTAC	3342
Db	3298	ACCAAGGCTGCTCTCCCTCCGTTCCCGGCGACGTGTTCAATGATTCGGCACTACGGCTAC	3357
Qy	3343	TAAAGCTCAACAAATGGCAGGCGAGGCAATGAGAGCTGATCTTTTACTGCTGGAATAT	3402
Db	3358	TAAAGCTCAACAAATGGCAGGCGAGGCAATGAGAGCTGATCTTTTACTGCTGGAATAT	3417
Qy	3403	TCCCATGCAAGATGCTGAGAACGGGCAATTAATCTTACCTTACACTACCTTCAGAGACG	3462
Db	3418	TCCCATGCAAGATGCTGAGAACGGGCAATTAATCTTACCTTACACTACCTTCAGAGACG	3477
Qy	3463	TGCTTTTCCACAGACGCTATGCGGCAACGCGACAGGCTTGAACCGGCTGATTAATCTCTCA	3522
Db	3478	TGCTTTTCCACAGACGCTATGCGGCAACGCGACAGGCTTGAACCGGCTGATTAATCTCTCA	3537
Qy	3523	TCGACCGATGCTGTATTTACTGTAACGAACTCAACATCTGATCCGGAAAGGCCCAAAACA	3582
Db	3538	TCGACCGATGCTGTATTTACTGTAACGAACTCAACATCTGATCCGGAAAGGCCCAAAACA	3597
Qy	3583	AGGACTTGCTGTTAGCGCGTGGGTCTTCAGCTGGCATGTCTGTTCAGGCCCAAAACTGGC	3642
Db	3598	AGGACTTGCTGTTAGCGCGTGGGTCTTCAGCTGGCATGTCTGTTCAGGCCCAAAACTGGC	3657
Qy	3643	TACCTGGAACCTGTATCCGCGCAGCGGCTTTCTAAATAAAGAAAGCAACAAACA	3702
Db	3658	TACCTGGAACCTGTATTCGCGCAGCGGCTTTCTAAATAAAGAAAGCAACAAACA	3717
Qy	3703	GCAACTTTACCTGGACTGTGCTTCAAAATATTAACCTTAATGGGCGGATCTATAATCA	3762
Db	3718	GCAACTTTACCTGGACTGTGCTTCAAAATATTAACCTTAATGGGCGGATCTATAATCA	3777
Qy	3763	ACCCTGGCACTGCTATGCTCTCAACAAAGACGCAAAAGCAAAAGTCTTTCCATGAGCG	3822
Db	3778	ACCCTGGCACTGCTATGCTCTCAACAAAGACGCAAAAGCAAAAGTCTTTCCATGAGCG	3837
Qy	3823	GTCGTATGATTTTGGAAAGAGAGCGCCGAGCTTCAACACTGCAATTTGGAACAATGTCA	3882
Db	3838	GTCGTATGATTTTGGAAAGAGAGCGCCGAGCTTCAACACTGCAATTTGGAACAATGTCA	3897
Qy	3883	TGATCACAGACGAAGAGAAATCAAAGCCACTAACCCCTGGGCGACCGAAAGATTTGGGA	3942
Db	3898	TGATCACAGACGAAGAGAAATTAAGCCACTAACCTGTGGCCACCGAAAGATTTGGGA	3957
Qy	3943	CTGTGGAGTCAATCTTCAGAGACGACGACAGCCCTGTGCGACCGGAGATGTGCATGTTA	4002
Db	3958	CTGTGGAGTCAATCTTCAGAGACGACGACAGCCCTGTGCGACCGGAGATGTGCATGTTA	4017
Qy	4003	TGGGAGCTTAACTTGGAATGCTGTGGCAABAACGAAACGTAATACCTGCAGAGGCTTAATT	4062
Db	4018	TGGGAGCTTAACTTGGAATGCTGTGGCAABAACGTAATACCTGCAGAGGCTTAATT	4077
Qy	4063	GGGCAAAATTTCTCAACAGGATGSAACATTTACCGGCTCTCTCTCATGGGCGCTTTG	4122
Db	4078	GGGCAAAATTTCTCAACAGATGSAACATTTACCGGCTCTCTCTCATGGGCGGCTTTG	4137
Qy	4123	GACTTAAGACCCGCTCTCTCAAGTCTCATCAAAAAACGCGCTGTTCTTGGCAATCTTC	4182

QY 583 CTTCCACCTCCATATTCTGTGTGAGACCA CGGGGTCAAAATC ATGTGCTGTGGCCGGCTT 642
Db 598 CTTCCACCTCCATATTCTGTGTGAGACCA CGGGGTCAAAATC ATGTGCTGTGGCCGGCTT 657
QY 643 CTTGATGATGATTAAGGCAAGCTGTGTGACCAATCTA CCGGGGATCGAGCCGACT 702
Db 658 CTTGATGATGATTAAGGCAAGCTGTGTGACCAATCTA CCGGGGATCGAGCCGACT 717
QY 703 GGGCAACTGTTCCGGGTGACCAAGA CGGTATATGGCGCGGAGGGGGGAA CAAGTGT 762
Db 718 GGGCAACTGTTCCGGGTGACCAAGA CGGTATATGGCGCGGAGGGGGGAA CAAGTGT 777
QY 763 GGAAGATGCTACATCCCAACTA CTTCTGCGCCCAAGACTGAGCCGAGCTGCA GTGGGC 822
Db 778 GGAAGATGCTACATCCCAACTA CTTCTGCGCCCAAGACTGAGCCGAGCTGCA GTGGGC 837
QY 823 GTGACATPAACATGAGAGATATATAGCGCTGTTTAAACCTGCGCCGAGCCAAACGCGCT 882
Db 838 GTGACATPAACATGAGAGATATATAGCGCTGTTTAAACCTGCGCCGAGCCAAACGCGCT 897
QY 883 CGTGGCGGACGACCTGACCCGACGTGACGCGACAGACCCAGAGAGCAACAAAGAAATCTGAA 942
Db 898 CGTGGCGGACGACCTGACCCGACGTGACGCGACAGACCCAGAGAGCAACAAAGAAATCTGAA 957
QY 943 CCCCATTCTGACGCGCTGTGATCCGGTCAAAAACTCCGACGCTACATGAGAGCTGGT 1002
Db 958 CCCCATTCTGACGCGCTGTGATCCGGTCAAAAACTCCGACGCTACATGAGAGCTGGT 1017
QY 1003 CGGGTGGCTGGTGAACCGGGGCACTCTCCGAGAGAGATGATCCAGAGAGACAGGC 1062
Db 1018 CGGGTGGCTGGTGAACCGGGGCACTCTCCGAGAGAGATGATCCAGAGAGACAGGC 1077
QY 1063 CTTGACATCTCTCTTCAACGCGCGCTCCAACTCGCGGTCCAGATCAAGGCGCGCTGGA 1122
Db 1078 CTTGACATCTCTCTTCAACGCGCGCTCCAACTCGCGGTCCAGATCAAGGCGCGCTGGA 1137
QY 1123 CAATGCGGCAAGATCATGAGCGCTGACCAAAATCCGCGCCGACCTACCTGTAGGCCCGCGC 1182
Db 1138 CAATGCGGCAAGATCATGAGCGCTGACCAAAATCCGCGCCGACCTACCTGTAGGCCCGCGC 1197
QY 1183 TCCGCGCGGCGACATTTAAACCAACCGGATTTACCGCATCTGAGAGCTGAAACGGCTACGA 1242
Db 1198 TCCGCGCGGCGACATTTAAACCAACCGGATTTACCGCATCTGAGAGCTGAAACGGCTACGA 1257
QY 1243 CCGTGCCTACGCGCGGCTCGTCTTTCTGCGCTGGGCGCCAGAAAAGTTCCGAAAAACGCA 1302
Db 1258 ACCTGCTACGCGCGGCTCGTCTTTCTGCGCTGGGCGCCAGAAAAGTTCCGAAAAACGCA 1317
QY 1303 CACCATCTGCTGTTTGGGCGCGGCAACGAGGCAAGACCAACATCCGAGAAAGCCATCGC 1362
Db 1318 CACCATCTGCTGTTTGGGCGCGGCAACGAGGCAAGACCAACATCCGAGAAAGCCATCGC 1377
QY 1363 CCAGCGCGTGGCTTTCTAGCGCTGCTCACTGGAACCAATGAGAACTTTCCCTTCAACGA 1422
Db 1378 CCAGCGCGTGGCTTTCTAGCGCTGCTCACTGGAACCAATGAGAACTTTCCCTTCAATGA 1437
QY 1423 TTTGGTGCACAAGATGTGATCTGGTGGGAGAGGGGCAAGATGA CCGGCAAGGTCTGGA 1482
Db 1438 TTTGGTGCACAAGATGTGATCTGGTGGGAGAGGGGCAAGATGAGCGCAAGGTCTGGA 1497
QY 1483 GTCCGCAAGGCACTTCTCGGCGGCAAGAGTGGCTGGAACCAAAAGTCAAGTCGTC 1542
Db 1498 GTCCGCAAGGCACTTCTCGGCGGCAAGAGTGGCTGGAACCAAAAGTCAAGTCGTC 1557
QY 1543 CGCCCAATTCATATCCCAACCCCGGTGATGTCACTTCCAAACCAACATGTGCGCGTGTAT 1602
Db 1558 CGCCCAATTCATATCCCAACCCCGGTGATGTCACTTCCAAACCAACATGTGCGCGTGTAT 1617
QY 1603 TGAAGGAAACAGACCACTTCCAGACCAAGAGCCGTTGAGAGACCGGATGTTCAATT 1662
Db 1618 TGAAGGAAACAGACCACTTCCAGACCAAGAGCCGTTGAGAGACCGGATGTTCAATT 1677
QY 1663 TGAACCTCAACCGCGCTGTGAGACATGACTTTGGCAAGGTGACAAAGACAGAAATCAAGA 1722

Db 1678 TGAACCTCAACCGCGCTGTGAGACATGACTTTGGCAAGGTGACAAAGACAGAAATCAAGA 1737
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Db 1738 GTTCTTCCGCTGGGCGGAGGATCAACGAGACGAGGTGGCCGACATGATCTTACGTCAGAAA 1797
QY 1783 GGGTGAAGCAACACAGACCCGCCGCCGATGACGCGGATAAAAAGCAGGCCAAGCGGGC 1842
Db 1798 GGGTGAAGCAACACAGACCCGCCGCCGATGACGCGGATAAAAAGCAGGCCAAGCGGGC 1857
QY 1843 CTGCCCCCTCAGTCGCGGATCCATGACGTGACAGCGGAAAGAGCTCCGTTGACTTTGC 1902
Db 1858 CTGCCCCCTCAGTCGCGGATCCATGACGTGACAGCGGAAAGAGCTCCGTTGACTTTGC 1917
QY 1903 CAGACGTTACCAAAACAAATGTTCTGTCACGCGGGGCACTCCTTCAGATGCTGTTCCCTG 1962
Db 1918 CAGACGTTACCAAAACAAATGTTCTGTCACGCGGGGCACTCCTTCAGATGCTGTTCCCTG 1977
QY 1963 CAAAACATGCGAGAGATGATCAGAAATTTCAACATTTGCTTACGCAACGAGCCAGAGA 2022
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QY 2023 CTGTTCAGAATGTTTCCCGGCGGTGACAAATCTCAACCGGTGTCAAGAAAGAGACTA 2082
Db 2038 CTGTTCAGAATGTTTCCCGGCGGTGACAAATCTCAACCGGTGTCAAGAAAGAGACTA 2097
QY 2083 TCCGAAATCTGAGGCAATTCATCATGCTGGGGCGGGGCTCCGAGATTGCTGTCCGCG 2142
Db 2098 TCCGAAATCTGAGGCAATTCATCATGCTGGGGCGGGGCTCCGAGATTGCTGTCCGCG 2157
QY 2143 CTGCGATCTGCTCAACGTGATCTGATGATGATCTGTTTCTGAGCAATTAATGA CTTAAAC 2202
Db 2158 CTGCGATCTGCTCAACGTGATCTGATGATGATCTGTTTCTGAGCAATTAATGA CTTAAAC 2217
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Db 2458 ACGACAGAGCTCAAAAGGGGGTGAACAATCGTAACTGGGTATTAACCAAGCCGACGCGC 2517
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Db 2518 AGTTTCAGAGCGCTCTGCAAGAAATACGCTTTTGGGGGCAACTCTCGGCGAGACGCTT 2577
QY 2563 TCCAGGCCAAGAGGGGTTCTGAACTTTTGGTCTGTTGAGAGAAAGTCTTAAGCGG 2622
Db 2578 TCCAGGCCAAGAGGGGTTCTGAACTTTTGGTCTGTTGAGAGAAAGGCTCTTAAGCGG 2637
QY 2623 CTTCTGGAAGAAACGTCGCGGTAGAGAGCGGCACAAGAGCCAGACTCTCTCTCGGGCA 2682
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Db 2758 CAGAGTCAGTCCCGGATCCAACTCTTCGAGAACTTCACAGACCCTCCGCTGCTG 2817
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Db 3418 TCCCATCGCAGATGCTGAGAACGGGCAATTAATTACCTTCACTACGCTTCGAGAG 3477
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Db 3478 TGCCTTTCCACAGCAGCTAGCGCAACGACCAAGCTTGAATGATCTCTCA 3537
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Db 3958 CCGTGGCAGTCAATTTCCAGAGCAGACAGACCGTCCGACCGGAGATGTCATGTTA 4017
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Db 4018 TGGAGCCTTACCTGGAATGCTGTGGCAAGACAGACGTAATACCTGCAAGGCTCTATT 4077
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Db 4198 CGGCGAGTCTTCAAGTCAAAAGTTTGCTTCAATCAACCAAGTATTCACAGACAA 4257
Qy 4243 TGAGCGTGAATGTAATGGAGCTGCAAGAAAGAAACAGAAACGCTGGAATCCCAAG 4302
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Qy 4541 -----ATACCCCTAGTGAAGTGGCCACTCCCTATGCGCGC 4581
Db 4557 AAAGACTTACGTATCGGGTTACCCCTAGTGAAGTGGCCACTCCCTCTGCGCGC 4616
Qy 4582 TCGCTGCTGGGTGGGCGCGCAGACAGACTTCCCGTGTGCGACCTTTGGTCCGA 4641
Db 4617 TCGCTGCTGGGTGGGCGCTGCGGACCAAGGTTCCGAGACGCGAGAGCTTGTCTGCC 4676
Qy 4642 GGCCCAACGAGCGAGCGGCGCATAGAGGGAGTGGCCAA 4683
Db 4677 GGCCCAACGAGCGAGCGGCGCATAGAGGGAGTGGCCAA 4718

RESULT 7
ADG39758
ID ADG39758 standard; DNA; 4718 BP.
XX
XX ADG39758;
XX
XX 11-MAR-2004 (first entry)
XX
XX AAV-1 genomic DNA sequence SHQ ID NO:20.
XX
XX parvovirus; rep; cap; DNA binding domain; capsid interacting domain;
XX recombinant hybrid parvovirus particle;
XX recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
XX gene; ds.

OS Adeno-associated virus 1.
XX MO2003104392-A2.
XX 18-DEC-2003.
XX 02-DEC-2002; 2002WO-US038423.
XX 18-DEC-2001; 2001US-0341919P.
XX (UTNC-) UNIV NORTH CAROLINA.
XX Samulek RJ, Rabinowitz JE;
XX WPI; 2004-062324/06.
XX
XX New polynucleotides comprising parvovirus rep coding sequences and
XX parvovirus cap coding sequences, useful in producing higher stocks of
XX hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
XX subject.
XX
XX Disclosure; SEQ ID NO 20; 115pp; English.
XX
XX The present invention describes a polynucleotide (I), comprising
XX parvovirus rep coding sequences and parvovirus cap coding sequences. The
XX rep coding sequences encodes a DNA binding domain from a first
XX parvovirus, and a capsid interacting domain from a parvovirus different
XX from the first parvovirus. The cap coding sequence comprises sequences
XX from the different parvovirus. Also described: (1) a vector comprising
XX (1); (2) a cell comprising (1), or parvovirus rep coding sequences and
XX parvovirus cap coding sequences, where the rep coding sequences encode a
XX DNA binding domain from a first parvovirus and a capsid interacting
XX domain from a parvovirus different from the first parvovirus, the cap
XX coding sequences comprise sequences from the different parvovirus, and
XX the rep coding sequences are stably integrated into the genome of the
XX cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
XX associated virus (rAAV) particle. (1) can be used in vaccines, and in
XX gene therapy. The polynucleotide (I) can be used in producing higher
XX stocks of hybrid parvoviruses or parvovirus vectors, which may be used in
XX the delivery of nucleic acids having biological effect to treat or
XX ameliorate the symptoms associated with any disorder related to gene
XX expression. The polynucleotide may be used to produce a parvovirus vector
XX to express an immunogenic polypeptide in a subject, e.g. for vaccination.
XX The parvovirus vector may also be used to provide an antisense nucleic
XX acid to a cell in vitro or in vivo, or in diagnostic and screening
XX methods. The present sequence is used in the exemplification of the
XX present invention.
XX
XX Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
SQ
Query Match 90.8%; Score 4253.2; DB 12; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;
QY 1 TTGGCCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCGCGGCGACCAAGCTGCC 60
DB 1 TTGGCCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCGCGGCGACCAAGCTGCC 60
QY 61 CGAGGCCCGGCGCTTTGCCCGGCGGCTCACTGAGCGAGCGCGGCGAGAGGAGTG 120
DB 61 AGAGCGGCGAGACTCTGCTCTGCTCCGCGCCACCGAGCGAGCGCGGCGAGAGGAGTG 120
QY 121 GCCAAGCTCATCACTAGAGGT-----TCTGAGGCGGCTGAGTCCGGA 163
DB 121 GCGAAGCTCATCACTAGAGGTATCGCGAAGCGCTCCACGCTGCCGCTCAGCGCTGA 180
QY 164 CGTGAATTACGTCATAGGCTTAGGAGGTCTGTATTAGAGTCACTGAGTG-TTTTGC 222
DB 181 CGTGAATTACGTCATAGG---GAGTGTCTGTATTAGTGTCACTGAGTGTGCTTTTGC 237
QY 223 GACATTTTGGCAGACCATGTGTGTCACGCTGGGTATTTAAGCCGAGTGAAGCAGAGGT 282
DB 238 GACATTTTGGCAGACCATGTGTGTCATTTAGGGTATTATGTGCGAGTGAAGCAGAGAT 297

QY 283 CTCATTTTGAAGCGGAGGTTTGAACGCGCAGCGCCATGCGCGGGTTTACGAGATTGT 342
DB 298 CTCATTTTGAAGCGGAGGTTTGAACGCGCAGCGCCATGCGCGGGTTTACGAGATTGT 357
QY 343 GATTAAAGTCCCGACGCACTTGAAGAGATCTGCCCGGATTTTGAAGCTTTGTGA 402
DB 358 GATCAAGTCCGACGCACTTGAAGAGATCTGCCCGGATTTTGAAGCTTTGTGA 417
QY 403 CTGGTGGCCGAGAAAGAAATGGAGTTGCCGAGATTTGAGATGGATCTGAT 462
DB 418 CTGGTGGCCGAGAAAGAAATGGAGTTGCCGAGATTTGAGATGGATCTGAT 477
QY 463 TGAGCAGGACCCCTGACCGGTGCCGAGAAAGTGCAGCGCACTTCTGCTCCACTGCG 522
DB 478 TGAGCAGGACCCCTGACCGGTGCCGAGAAAGTGCAGCGCACTTCTGCTCCAAATGGCG 537
QY 523 CCGGTGAGTGAAGCGCCCGGAGCGCTCTTTCTTTGTTCACTTGAAGAGGCGAGTCTTA 562
DB 538 CCGGTGAGTGAAGCGCCCGGAGCGCTCTTTCTTTGTTCACTTGAAGAGGCGAGTCTTA 597
QY 583 CTTCCAACTCATATTCTGTGTGAAGCAAGGGGTCAAATTCATAGTGTGTGGCCGCTT 642
DB 598 CTTCCAACTCATATTCTGTGTGAAGCAAGGGGTCAAATTCATAGTGTGTGGCCGCTT 657
QY 643 CTGAGTCAAGATTAGCAGCAAGCTGTGACAGCACTTACCGCGGATCGAGCCGACCTT 702
DB 658 CTGAGTCAAGATTAGCAGCAAGCTGTGACAGCACTTACCGCGGATCGAGCCGACCTT 717
QY 703 GCCCAATGTTGTCGCGGTGACCAAGACGCTAATGCGCCGAGGGGGCAAGAGTGTGT 762
DB 718 GCCCAATGTTGTCGCGGTGACCAAGACGCTAATGCGCCGAGGGGGCAAGAGTGTGT 777
QY 763 GAGCAGTGTATATCCCACTACCTCCGCCAAGACTCAGCCGAGCTGAGTGGGC 822
DB 778 GAGCAGTGTATATCCCACTACCTCCGCCAAGACTCAGCCGAGCTGAGTGGGC 837
QY 823 GTGACATTAATGAGAGGATATTAAGCGCGTATTAACCTTGGCCGAGCGCAAGCGCT 882
DB 838 GTGACATTAATGAGAGGATATTAAGCGCGTATTAACCTTGGCCGAGCGCAAGCGCT 897
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DB 958 CCCCAATTGAGAGCGCGCTGATCCGCGTCAAAAACCTCCGCGCTACATGAGCTGGT 1017
QY 1003 CGGCTGCTGTGAGACCGGGGCACTCACTCCGAGAAAGCAATGATCCAGAGGACCAAGG 1062
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DB 1198 TCCGCCCGCAGCAATTAAACCAACGCACTTACCGGATCTGAGGTGAACCGCTTACGA 1257
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DB 1258 ACCTGTCTACGCGCGCTCGCTCTTTCTGCGCTGGGCCAGAAAAAGTTCCGAAAAACGCA 1317
QY 1303 CACCATCTGGCTGTTTGGGCGCGGCAACCAAGGCAAGAACCAATGCGGAGGCAATGCG 1362
DB 1318 CACCATCTGGCTGTTTGGGCGCGGCAACCAAGGCAAGAACCAATGCGGAGGCAATGCG 1377

Qy 1363 CCACGCGTGCCTTCTACGGCTGCCTCACTGACCAATGAGAACTTTCCCTTCAAGCA 1422
Db 1378 CCAAGCCCTGCTCTTCTACGGCTGCCTCACTGACCAATGAGAACTTTCCCTTCAAGCA 1437
Qy 1423 TTGCGTCGACAAAGATGATGATCTGATGGAGAGAGGCAAGATGACGGCCAAAGTGTGGA 1482
Db 1438 TTGCGTCGACAAAGATGATGATCTGATGGAGAGAGGCAAGATGACGGCCAAAGTGTGGA 1497
Qy 1483 GTCCGCGCAAGGCCAATTTCTCGCGCGGACGACAGATGGCGCTGTGACCAAAAGTCAAGTCTTC 1542
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Qy 1543 CGCCAGATGATCCACCCCGGTGATGTCACCTCCAAACCAATGATGTGCGCGGTAT 1602
Db 1558 CGCCAGATGATCCACCCCGGTGATGTCACCTCCAAACCAATGATGTGCGCGGTAT 1617
Qy 1603 TGACGGGAAACAGCACACCTTTCAGACACGACGCGTTGACAGGACCGGATGTTCAAAAT 1662
Db 1618 TGACGGGAAACAGCACACCTTTCAGACACGACGCGTTGACAGGACCGGATGTTCAAAAT 1677
Qy 1663 TGAATCTCACCCGCGCTCTGAGACATGACTTTTGGCAAGTGACAAAGCAAGTCAAAAGA 1722
Db 1678 TGAATCTCACCCGCGCTCTGAGACATGACTTTTGGCAAGTGACAAAGCAAGTCAAAAGA 1737
Qy 1723 GTTCTTCCGCTGGGCGCAGATCAGTGAACGAGGTGGCGCATGATTTCTACGTCAAAA 1782
Db 1738 GTTCTTCCGCTGGGCGCAGATCAGTGAACGAGGTGGCGCATGATTTCTACGTCAAAA 1797
Qy 1783 GGGTGGAGCCAAACAGACAGCCGCCCGATGACCGGATAAAGCGAGCCCAAGCGGGC 1842
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Qy 1903 CGACAGATACCAAAACAATGTTCTGTCAGCGGGGACGTCTTCAGATGCTGTTCCCTG 1962
Db 1918 CGACAGATACCAAAACAATGTTCTGTCAGCGGGGACGTCTTCAGATGCTGTTCCCTG 1977
Qy 1963 CAAAACATGCGAGAGATGAAATCAAGAAATTTCAACTTTGCTTTCAGCAGCGGACCGAGGA 2022
Db 1978 CAAAACATGCGAGAGATGAAATCAAGAAATTTCAACTTTGCTTTCAGCAGCGGACCGAGGA 2037
Qy 2023 CTGTTTCAAGATGTTTCCCGCGGTCTCAAGATCTCAACCGGTCTCAAGAAAGAGAGCTTA 2082
Db 2038 CTGTTTCAAGATGTTTCCCGCGGTCTCAAGATCTCAACCGGTCTCAAGAAAGAGAGCTTA 2097
Qy 2083 TCGGAACCTGTGTCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTTGCTGTGGC 2142
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Qy 2143 CTGCGATCTGATCAACGTGATCTGATGATCTGATGATCTGATGATGATGATGATGATGAT 2202
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Qy 2203 CAGGATATGCTGCGCATGATGATCTTCAAGATGATGATGATGATGATGATGATGATGAT 2262
Db 2218 CAGGATATGCTGCGCATGATGATCTTCAAGATGATGATGATGATGATGATGATGATGAT 2277
Qy 2263 TTTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2322
Db 2278 TTTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2337
Qy 2323 AGGACGACGCGCGGGTCTGATGATCTTCTGATCAAGATGATGATGATGATGATGATGATGAT 2382
Db 2338 AGGACGACGCGCGGGTCTGATGATCTTCTGATCAAGATGATGATGATGATGATGATGATGAT 2397
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Db 2518 AGTTTCAAGAGCGTCTGACAAAGATAGCTTTTGGGGGCAACTCGGCGAGACATCT 2577
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Qy 2743 CAGAGTCAATCCCGACCCCAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGG 2802
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Qy 2923 TCAATCAACACAGACACCCGAACATGGGCTTTGCCACTATTAACAACCTCTCAAGC 2982
Db 2938 TCAATCAACACAGACACCCGAACATGGGCTTTGCCACTATTAACAACCTCTCAAGC 2997
Qy 2983 AAATCTCAAGTCTTCAACGGGGGCGCAGCAAGCAACCACTACTTGGCTACAGACCC 3042
Db 2998 AAATCTCAAGTCTTCAACGGGGGCGCAGCAAGCAACCACTACTTGGCTACAGACCC 3057
Qy 3043 CTTGGGGGTATTTTATTTCAACAGATTCACCTCCATTTCTCAACAGTGAATGGCAGC 3102
Db 3058 CTTGGGGGTATTTTATTTCAACAGATTCACCTCCATTTCTCAACAGTGAATGGCAGC 3117
Qy 3103 GACTCATCAACAATAATTTGGGATTTCCGGCCCAAGAGATCAACTCAAGCTCTCAACA 3162
Db 3118 GACTCATCAACAATAATTTGGGATTTCCGGCCCAAGAGATCAACTCAAGCTCTCAACA 3177
Qy 3163 TCCAAATCAAGAGAGTCAAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 3222
Db 3178 TCCAAATCAAGAGAGTCAAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 3237
Qy 3223 GCACGGTTCAAGTCTTGTGAGACTCGGAGTACAGATTCGCGTACGTCTCGGCTCTGCGC 3282
Db 3238 GCACGGTTCAAGTCTTGTGAGACTCGGAGTACAGATTCGCGTACGTCTCGGCTCTGCGC 3297
Qy 3283 ACAGGGCTGCTCTCTCCGTTCCCGGCGACGTTTCAAGATTTCCGCAAGTACGCGCTAAC 3342
Db 3298 ACAGGGCTGCTCTCTCCGTTCCCGGCGACGTTTCAAGATTTCCGCAAGTACGCGCTAAC 3357
Qy 3343 TTAACGCTCAACAAATGGGAGCAGAGCAGTGGGAGCTCATCTTTTACTGCTGAGATATT 3402
Db 3358 TTAACGCTCAACAAATGGGAGCAGAGCAGTGGGAGCTCATCTTTTACTGCTGAGATATT 3417
Qy 3403 TCCGATCGCAGATGCTGAGAACGGGCAATACTTTTACTGCTGAGATATT 3462
Db 3418 TCCGATCGCAGATGCTGAGAACGGGCAATACTTTTACTGCTGAGATATT 3477
Qy 3463 TGCCTTTTCCACAGAGCTTACGCGACAGCAGAGCTGAGACCGGCTGATGATGATGATGAT 3522
Db 3478 TGCCTTTTCCACAGAGCTTACGCGACAGCAGAGCTGAGACCGGCTGATGATGATGATGAT 3537
Qy 3523 TCGACCAAGTACTGTATTTTACTGTAACAGAACTCAACTCAAGTCCGGAAGTCCCAAAACA 3582

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Dh 3538 TCACCAATACCTGTATTACCTGAACAGAACTCAAAATCACTGCGAAGTCCCAAAACA 3597
Oy 3583 AGACCTGCTGTTTAGCCGTGGTCTCCAGCTGGAGTGTCTGTTGAGCCCAAAACTGGC 3642
Dh 3598 AGGACTGCTGTTTAGCCGTGGTCTCCAGCTGGAGTGTCTGTTGAGCCCAAAACTGGC 3657
Oy 3643 TACCTGACCCCTGTTACCGGAGCAGCGCGCTTTCAAAACAAAACAGACAACAACA 3702
Dh 3658 TACCTGACCCCTGTTATGCGAGGAGCGCGTTTCAAAACAAAACAGACAACAACA 3717
Oy 3703 GCAACTTACCTGAGCTGTGCTTCAAAATATACTTAATAGGCGGTAACTCTAATCA 3762
Dh 3718 GCAATTTTACCTGAGCTGTGCTTCAAAATATACTTAATAGGCGGTAACTCTAATCA 3777
Oy 3763 ACCCTGAGCTGCTATGCTCACAACAAGACAAAGACAAAGTCTTCTCCATGAGCG 3822
Dh 3778 ACCCTGAGCTGCTATGCTCACAACAAGACAAAGACAAAGTCTTCTCCATGAGCG 3837
Oy 3823 GTGTATGATTTTGGAAAGAGAGCGCGGAGCTTCAAAACATGCAATTTGACAATGCA 3882
Dh 3838 GTGTATGATTTTGGAAAGAGAGCGCGGAGCTTCAAAACATGCAATTTGACAATGCA 3897
Oy 3883 TGATCAGCAGAGAGAGAGAAATCAAAAGCCTAAACCCCTGTGCGCACCGAAATTTGGGA 3942
Dh 3898 TGATTTACAGAGAGAGAGAAATTAAGCCACTAACCCCTGTGCGCACCGAAATTTGGGA 3957
Oy 3943 CTGTGAGCAGTCAATCTCCAGAGCAGCAGACAGACCTGTGCGCAGAGATGTGATGTTA 4002
Dh 3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGACAGACCTGTGCGCAGAGATGTGATGTTA 4017
Oy 4003 TGGAGCCTTACCTGGAATGCTGTGCAAGACAGAGCGTATACCTGAGGCTCTAATTT 4062
Dh 4018 TGGAGCCTTACCTGGAATGCTGTGCAAGATAGAGAGTGTACCTGAGGCTCTAATTT 4077
Oy 4063 GGGCCAAAATTCCTCACAOGATGAGACCTTCAACCCCTCTCTCTCAATGGCGGCTTTG 4122
Dh 4078 GGGCCAAAATTCCTCACAOGATGAGACCTTCAACCCCTCTCTCTTAAATGGCGGCTTTG 4137
Oy 4123 GACTTAAGCAGCCGCTCTCAGATCTCATCAATAAACAACCCCTGTGCTCTGATCTCTC 4182
Dh 4138 GACTCAGAACCCGCTCTCTCAGATCTCATCAATAAACAACCCCTGTGCTCTGATCTCTC 4197
Oy 4183 CGGAGAGTCTTTCGGCTACAAAGTTTGCTTCAATTCATCAACCCAGTATTCACAGACAA 4242
Dh 4198 CGGCGAGATTTTCAGCTCAAAAGTTTGCTTCAATTCATCAACCCAGTATTCACAGACAA 4257
Oy 4243 TGAGCTGAGATTTGAATGGAGCTGCAAGAAAGAAACAGAAACGCTGGAATCCCGAAG 4302
Dh 4258 TGAGCTGAGATTTGAATGGAGCTGCAAGAAAGAAACAGAAACGCTGGAATCCCGAAG 4317
Oy 4303 TGCAGTATACATCTTAATATGCAAAATCTGCCAAGCTTGAATTTCACTGTGACAACAATG 4362
Dh 4318 TGCAGTATACATCTTAATATGCAAAATCTGCCAAGCTTGAATTTCACTGTGACAACAATG 4377
Oy 4363 GACTTATATGAGCTTCCGCTTGGACCCGCTTACCTCAACCCGCTCCCTGTAAATGT 4422
Dh 4378 GACTTATATGAGCTTCCGCTTGGACCCGCTTGGACCCGCTTACCTCAACCCGCTCCCTGTAAATG 4437
Oy 4423 GTGTATATCAATAAACCGGTTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4482
Dh 4438 GTGTATATCAATAAACCGGTTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4497
Oy 4483 TCTTATCTGTACCATAGCAACCGGTTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4540
Dh 4498 TCTTATCTGTACCATAGCTTAATGCTTAACATTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4556
Oy 4541 TCTTATCTGTACCATAGCTTAATGCTTAACATTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4581
Dh 4557 TCTTATCTGTACCATAGCTTAATGCTTAACATTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4616
Oy 4582 TCTTATCTGTACCATAGCTTAATGCTTAACATTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4641
Dh 4617 TCTTATCTGTACCATAGCTTAATGCTTAACATTAATCTGTGCTGAGTGAACCTTGGCTATATGCTCTAATTA 4676
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Oy 4642 GGCCCCACGAGGAGCGAGCGGCAATAGAGGAGTGGCCA 4683
Dh 4677 GGCCCCACGAGGAGCGAGCGGCAAGAGGAGTGGCCA 4718

RESULT 8
ADM39402
ID ADM39402 standard; DNA; 4239 BP.
XX
AC ADM39402;
XX
XX 24-MAR-2005 (first entry)
XX
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 5.
XX
XX genetically engineered microorganism; vector; rep; cap; ds.
XX
XX Adeno-associated virus 2.
OS Chimeric.
OS Unidentified.
XX
XX CN1461805-A.
XX
XX 17-DEC-2003.
XX
XX 27-MAY-2002; 2002CN-00117965.
XX
XX 27-MAY-2002; 2002CN-00117965.
XX
XX (BENYU) BENYUAN ZHENGYANG GENETIC TECHNOLOGY CO.
XX
XX Mu X, Cao H, Dong X;
XX
XX WPI; 2004-248658/24.
XX
XX Structure of a recombinant herpes simplex virus and its use.
XX
XX Claim 5; SEQ ID NO 5; 102pp; Chinese.
XX
XX The invention relates to a novel recombinant herpes simplex virus (rHSV)
XX whose genome is respectively inserted by the Adeno-associated virus (AAV)
XX rep gene and cap gene. The AAV genes may be derived from viruses AAV1,
XX AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
XX useful for generating recombinant vectors with high efficiency and no
XX need of reconfiguration. The current sequence is that of the Adeno-
XX associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
XX DNA (SEQ ID 5) of the invention.
XX
XX Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;
XX
XX Best Match 81.8%; Score 3831.4; DB 13; Length 4239;
XX Query Locality 94.3%; Pred. No. 0;
XX Matches 3997; Conservative 0; Mismatches 236; Indels 4; Gaps 2;

Oy 191 GTCTGTATTTAAGAGTCACTGAGTGTGTTTGCAGATTTTGCAGACCATGTGTCACGC 250
Dh 6 GTCTGTATTTAAGAGTCACTGAGTGTGTTTGCAGATTTTGCAGACCATGTGTCACGC 65
Oy 251 TGGGTATTTTAAGCCCGAGTGAAGCAGAGGCTCTCCATTTTGAAGCGGAGTTTGAACG 310
Dh 66 TGGGTATTTTAAGCCCGAGTGAAGCAGAGGCTCTCCATTTTGAAGCGGAGTTTGAACG 125
Oy 311 CGCAG-CGCCATGCGGAGTTTGAAGATTTGATTAAGTCCCGCAGCAGCTTGAACA 369
Dh 126 CGCAGCCGCAATGCGGAGTTTGAAGATTTGATTAAGTCCCGCAGCAGCTTGAACA 185
Oy 370 GCATCTGCCCGGCAATTTCTGACAGCTTTGTGAATCTGGTGGCGGAGAAATGGAGTT 429
Dh 186 GCATCTGCCCGGCAATTTCTGACAGCTTTGTGAATCTGGTGGCGGAGAAATGGAGTT 245
Oy 430 GCGCCGAGATTTCTGACATGATCTGAATCTGATTTGAGCAGCAGCCTGACCGTGGCGGA 489
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Db 246 GCCGCAGATTCTGACATGGAATCTGAAATCTGATTGAGCAGGACCCCTGATCCGTGAGCGA 305
Qy 490 GAAGCTGACGAGCGGACTTCTCTGCTCACTGAGCGCGGAGTAAAGGCCCGGAGAGCCCT 549
Db 306 GAAGCTGACGAGCGGACTTCTCTGAGAGTGGCGCGGTGAGATTAAGGCCCGGAGAGCCCT 365
Qy 550 CTTCTTTTGTTCAGTTGAGAAAGGAGGAGCTTACTTCCACTTCCATTAATTTCTGTGAGAGC 609
Db 366 TTTCTTTGTGCAATTGAGAAAGGAGAGAGCTACTTCCACATGCAAGTCTGTGTGAAAC 425
Qy 610 CACGGGGGTCAAAATCCATGTGTCTGAGCGCTTCTCTGAGTCAAGATTAGCGACAAGCTGT 669
Db 426 CACCGGGGTGAATCATGTGTTTGGGAGCGTTTCTGAGTCAAGATTCCGGAAAACTGAT 485
Qy 670 GCAGACCATCTACCGCGGGATGAGCCGACCCCTGCGCAATGCTTCCGGGTGACCAAGAC 729
Db 486 TCAGGAATTTACCCCGGATGAGCCGACTTTGCGCAACCTGTTCCGGGTGACCAAGAC 545
Qy 730 GCGTAATGAGCGCGAGGGGGGAGCAAGGTGTGACGAGTCTACATCTCCCACTACT 789
Db 546 CAGAAATGGCGCGAGGGGGGAGCAAGGTGTGATGAGTCTACATCTCCCACTACT 605
Qy 790 CCTGCTCCAAAGACTACGCCGAGCTGAGTGGCGGTGACTAAATGAGAGAGATATTAAG 849
Db 606 GCTCCCAAAACCCAGCTGAGCTCAGTGGCGGTGACTAATATGAAACAGTATTTAAG 665
Qy 850 GCGGTGTTTAAACCTGGCGAGCGGCAACGCGTCTGCGCGGACGACCTGACCCAGCTGAG 909
Db 666 GCGCTGTTGAATCTCAAGAGCGGTAACGCTTGTGGCGGAGCACTGACGACAGTGTG 725
Qy 910 CCAGACCCAGAGAGCAGAAACAGAGAAATCTGAACCCCAATTTGACGCGCTGTATCCG 969
Db 726 GCAAGCGAGAGAGCAAGAAAGAAATCCCAATTTGATGAGCGCGGTGATCAG 785
Qy 970 GTCAAAAACCTCCGACCGCTCATGAGCTGTGTGGGTGTGAGTGAACGGGGCATCAC 1029
Db 786 ATCAAAAACCTTCAGCAGATCATGAGCTGTGTGGGTGTGAGTGAACGGGGATTAAC 845
Qy 1300 CTCGAGAAAGAGTGGATCCAGAGAGACAGGCGCTCGTAACATCTCTTCAACCGGCTTC 1089
Db 846 CTCGAGAAAGAGTGGATCCAGAGAGACAGGCGCTCGTAACATCTCTTCAACCGGCTTC 905
Qy 1090 CAACCTCGGCTCCAGATCAAGGCGCTCTGGAACATGCGGCAAGATCATGAGCTGAC 1149
Db 906 CAACCTCGGCTCCAGATCAAGGCGCTCTGGAACATGCGGAAAGATTAGAGCTGAC 965
Qy 1150 CAATTCGCGCCCGACTACTGTGAGGCGCGCTCCGCGCGCAATTAACCAACCG 1209
Db 966 TAAAAACCGCCCGACTACTGTGAGGCGCGCTCCGCGCGCAATTAACCAACCG 1025
Qy 1210 CATTTACCGCATCTCTGAGCTGAAAGGCTACGACCTTGGCTTACCGCGCTCTCTTCT 1269
Db 1026 GATTATTAATAATTTTGAACATAAGGGTACGATCCCAATATGCGCTTCCGTCTTCT 1085
Qy 1270 CGGCTGGGCGCAGAAAAAGTTTCGGAACAGCAACCATCTGCTTTTGGCGGCGCAC 1329
Db 1086 GGGATGGGCGCAGAAAAAGTTTCGGAACAGCAACCATCTGCTTTTGGCGGCGCAC 1145
Qy 1330 CACGGGCAAGCAACATCGCGGAAGCCATGCGCCAGCGCGCTTCTTACCGCTGCT 1389
Db 1146 TACCGGGAGAACCAATCGCGAGGCCATAGCCACACTGTGCCCTTCTACGGGTGCT 1205
Qy 1390 CAACCTGACCAATGAGAACTTTCCCTTCAAGATTGGCTGACAAAGATGGATCTGTG 1449
Db 1206 AATCTGACCAATGAGAACTTTCCCTTCAAGATCTGTGACAAAGATGGATCTGTG 1265
Qy 1450 GAGAGAGGCAAGATGAGAGCGCAAGTGTGAGTCCGCAAGGCAATTTCTGCGCGCAG 1509
Db 1266 GAGAGAGGCAAGATGAGAGCGCAAGTGTGAGTCCGCAAGGCAATTTCTGCGGAGAG 1325
Qy 1510 CAAGTGTGCTGTGACCAAAAGTGTGATGCTCGCGCCAGATCGATCCCAACCGCGTAT 1569
Db 1326 CAAGTGTGCTGTGACCAAAAGTGTGATGCTCGCGCCAGATCGATCCCAACCGCGTAT 1385

Qy 1570 GGTCACTTCAACACCAATGTGCGCGGTGATTGAGGGGAACAGCACACCTTGTAGCA 1629
Db 1386 GGTCACTTCAACACCAATGTGCGCGGTGATTGAGGGGAACAGCACACCTTGTAGCA 1445
Qy 1630 CCAGCAGCGGTGAGAGACCGGATGTTCAATTTGAACTCACCCGCGCTGTGAGCATGA 1689
Db 1446 CCAGCAGCGGTGAGAGACCGGATGTTCAATTTGAACTCACCCGCGCTGTGAGCATGA 1505
Qy 1690 CTTTGGCAAGGTGACAAAGCAGAAAGTCTTCCGCTGGCGCGCAGATCACT 1749
Db 1506 CTTTGGGAAGGTGACAAAGCAGAAAGTCTTCCGCTGGCGCGCAGATCACT 1565
Qy 1750 GACCGAGGTGCGCATGAGTCTACGTGAGAAAGGTGAGACCAACACACCGCGCC 1809
Db 1566 GATTGAGGTGAGCATGAAATTTCTACGTCAAAAAGGTGAGACCAAAAACCGCGCC 1625
Qy 1810 CGATGACCGGATTAAGAGCAGACCGGCGCTGACCTCAAGTCCGAGTCCATCGAC 1869
Db 1626 CAGTACCGCATATTAAGTGAAGCCCAACGGGTGCGGAGTCCGAGCCATCGAC 1685
Qy 1870 GTCAAGCGGGAAGAGCTCCGTGAGACTTTCGAGCAGGTACCAAAACAAATGTTCTG 1929
Db 1686 GTCAAGCGGGAAGAGCTCCGTGAGACTTTCGAGCAGGTACCAAAACAAATGTTCTG 1742
Qy 1930 TCAGCGGGGCAATGCTTCAAGTGTCTCCCTGCAAAACAGCGAGAGAAATGACAA 1989
Db 1743 TCAGCGGGGCAATGCTTCAAGTGTCTCCCTGCAAAACAGCGAGAGAAATGACAA 1802
Qy 1990 TTTCAACATTTGCTTCAACGACGAGGACAGAGCTGTTCAAGATGTTTCCCGCGGTG 2049
Db 1803 TTTCAACATTTGCTTCAACGACGAGGACAGAGCTGTTCAAGATGTTTCCCGCGGTG 1862
Qy 2050 AGAATTCACCGGTGCTCAGAAAGAGAGCTATCGGAACTCTGTGCAATCATCT 2109
Db 1863 AGAATTCACCGGTGCTCAGAAAGAGAGCTATCGGAACTCTGTGCAATCATCT 1922
Qy 2110 GCTGGGGGGGCTCCGAGATGCTTGTGCGCGCTGAGTGTGCAACGTTGATCGGA 2169
Db 1923 GCTGGGGGGGCTCCGAGATGCTTGTGCGCGCTGAGTGTGCAACGTTGATCGGA 1982
Qy 2170 TGACTGTGTTCTGAGCAATTAATGACTTAACCAAGATATGCTGCGGATGTTATCTTC 2229
Db 1983 TGACTGTGTTCTGAGCAATTAATGACTTAACCAAGATATGCTGCGGATGTTATCTTC 2042
Qy 2230 CAGATTGGCTGAGGACAACTCTCTGAGGCAATTCGAGGTGTGGAACCTTG 2289
Db 2043 CAGATTGGCTGAGGACAACTCTCTGAGGCAATTCGAGGTGTGGAACCTTG 2102
Qy 2290 GAGCGCGGAAACCCAAAGCCAACAGCAAAAGCAGAGCGCGGGGTCTGGTGTTC 2349
Db 2103 GAGCGCGGAAACCCAAAGCCAACAGCAAAAGCAGAGCGCGGGGTCTGGTGTTC 2162
Qy 2350 CTGCTCAAGTACTCTGAGACCTTCAACGGACTCGAACAGGGGGAACCGTCAACCGG 2409
Db 2163 CTGCTCAAGTACTCTGAGACCTTCAACGGACTCGAACAGGGGGAACCGTCAACCGG 2222
Qy 2410 CGGATGAGGGGCGCTTGAGACGACAAAGGCTTACGACGAGAGCTCAAAAGCGGTGACA 2469
Db 2223 CGGATGAGGGGCGCTTGAGACGACAAAGGCTTACGACGAGAGCTCAAAAGCGGTGACA 2282
Qy 2470 ATCCGTACTGCGGTATTAACGAGCGGACCGCGAGTTTCAAGGAGCGTCAAGAAATA 2529
Db 2283 ATCCGTACTGCGGTATTAACGAGCGGACCGCGAGTTTCAAGGAGCGTCAAGAAATA 2342
Qy 2530 GGTCTTTTGGGGGCAACCTCGGGGAGCAAGTCTTCCAGGCGCAAGAGAGGTTCTCGAC 2589
Db 2243 GGTCTTTTGGGGGCAACCTCGGGGAGCAAGTCTTCCAGGCGCAAGAGAGGTTCTCGAC 2402
Qy 2590 CTTTGTGTGTGTGAGGAAGGTGCTTAAGACGCTCTGTGAAAGAAACGTTCCGTTAGAC 2649
Db 2403 CTTTGTGTGTGTGAGGAAGGTGCTTAAGACGCTCTGTGAAAGAAACGTTCCGTTAGAC 2462

OY	2650	AGTGGCCACAAAGACGACATCTCTCTCTGGGCATTTGGCAGACAGGCCAGCACC	CGCTA	2709
Db	2463	AGTGGCCACAAAGACGACATCTCTCTCTGGGCATTTGGCAGACAGGCCAGCACC	CGCTA	2522
OY	2710	AAAAGAGCTCAATTTTGGTCAGATGGCCGACTCAGAGTCAAGTCCCGACC	CAACCTC	2769
Db	2553	AAAAGAGCTCAATTTTGGTCAGAGTCCCGACTCAGAGTCAAGTCCCGACC	CAACCTC	2582
OY	2770	TGGGAAACCTTCAGCAACCCCCGCTGCTGGGACCTTACTCAATGGCTTCAG	CGGTG	2829
Db	2583	TGGGAAACCTTCAGCAACCCCCGCTGCTGGGACCTTACTCAATGGCTTCAG	CGGTG	2642
OY	2830	GGCGACCAATGGCAGACAAATAACGAGCGCCGACGAGTGGGTATATGCTC	CAGAAATT	2889
Db	2643	GGCGACCAATGGCAGACAAATAACGAGCGCCGACGAGTGGGTATATGCTC	CAGAAATT	2702
OY	2890	GGCATTTGGATTTCCACATGGCGTGGGCGCAGAGTCATACCAACGACGCC	GAATGGG	2949
Db	2703	GGCATTTGGATTTCCACATGGCGTGGGCGCAGAGTCATACCAACGACGCC	GAATGGG	2762
OY	2950	CCTTGGCCACCTATTAACAACACACTCTTAACAAGCAATCTCCAGTCTT	CAACGGGGCCA	3009
Db	2763	CCTTGGCCACCTATTAACAACACACTCTTAACAAGCAATCTCCAGTCTT	CAACGGGGCCA	2822
OY	3010	GCAACGACAAACCACTACTTGGCTTACAGACACCCCTGGGGGTATTTT	GATTTCAACGAT	3069
Db	2823	GCAACGACAAACCACTACTTGGCTTACAGACACCCCTGGGGGTATTTT	GATTTCAACGAT	2882
OY	3070	TTCCATGTCATTTTCTCACACGTGACTGGCAGCGACTCATCAACAACA	ATTGGGGATTCC	3129
Db	2883	TTCCATGTCATTTTCTCACACGTGACTGGCAGCGACTCATCAACAACA	ATTGGGGATTCC	2942
OY	3130	GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCTCAAGTCAAGAG	AGGTTCACGACGATG	3189
Db	2943	GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCTCAAGTCAAGAG	AGGTTCACGACGATG	3002
OY	3190	ATGGCGTCAACCACTGCTATTAATACTTACACGACGGTTCAAAGTCT	TGTCGGACTCGG	3249
Db	3003	ATGGCGTCAACCACTGCTATTAATACTTACACGACGGTTCAAAGTCT	TGTCGGACTCGG	3062
OY	3250	AGTACCAATTCCTCGATAGCTCGCTGGGCTGCGACACAGGGCTGCTC	CTCGTTCCCGG	3309
Db	3063	AGTACCAATTCCTCGATAGCTCGCTGGGCTGCGACACAGGGCTGCTC	CTCGTTCCCGG	3122
OY	3310	CGGACGTGTGATGATTCGCGAGTACGGCTTACTTAACGCTCAACAT	TGGCCAGGACG	3369
Db	3123	CGGACGTGTGATGATTCGCGAGTACGGCTTACTTAACGCTCAACAT	TGGCCAGGACG	3182
OY	3370	TGGGACGCTACTCTTTTACTGCTGTGAATAATTTCCATGCGACAGT	GTGGAACGGGCA	3429
Db	3183	TGGGACGCTACTCTTTTACTGCTGTGAATAATTTCCATGCGACAGT	GTGGAACGGGCA	3242
OY	3430	ATTAACCTTAACCTTCAGCTACACCTTTCGAGGACGTGCCCTTTC	ACACAGACGCTACCGGCA	3489
Db	3243	ATTAACCTTAACCTTCAGCTACACCTTTCGAGGACGTGCCCTTTC	ACACAGACGCTACCGGCA	3302
OY	3490	GCCAGAGCCTGGACCGGCTGATGATCTCTTCATCGACACAGTAC	CTGTATTAACCTGAACA	3549
Db	3303	GCCAGAGCCTGGACCGGCTGATGATCTCTTCATCGACACAGTAC	CTGTATTAACCTGAACA	3362
OY	3550	GAACCTCACAAATCAGTCGCGAAAGTGCACAAACAGAGCTTGT	GTATAGCCGTGGGTCTC	3609
Db	3363	GAACCTCACAAATCAGTCGCGAAAGTGCACAAACAGAGCTTGT	GTATAGCCGTGGGTCTC	3422
OY	3610	CAGCTGGCATGTCTGTTCAGCCCAAAAATGCGCTTACCTGGA	CCCTGTTACCGGACGACG	3669
Db	3423	CAGCTGGCATGTCTGTTCAGCCCAAAAATGCGCTTACCTGGA	CCCTGTTACCGGACGACG	3482
OY	3670	GGCTTTCTAAAAACAACAAACAGACAAACAACAGCACTTTT	ACCTGGACCTGGTCTTCAA	3729
Db	3483	GGCTTTCTAAAAACAACAAACAGACAAACAACAGCACTTTT	ACCTGGACCTGGTCTTCAA	3542
OY	3730	AATATTAACCTTAATGGGCGTGAATCTATATCAACCTTGG	ACTTGGCTTCAACA	3789

[illegible]

PA (AGTC-) AGTC GENE TECHNOLOGY CO LTD.
 XX Mu X, Cao H, Dong X;
 XX WPI; 2005-296279/30.
 XX Large-scale production, isolation and purification of serotype adeno-
 PT associated virus vectors by infecting cells with recombinant herpes
 PT simplex virus vectors, for use in gene therapy of e.g. cancer and
 PT respiratory diseases.
 XX Claim 1; SEQ ID NO 5; 79pp; Chinese.
 XX The invention relates to a recombinant herpes simplex virus (HSV)
 CC characterized in that its genome is inserted with a DNA sequence selected
 CC from nucleotide sequences of AD246594-AD246598 or their homologous
 CC sequences. Also included are preparing the recombinant HSV (comprising
 CC the construction of DNA fragments that contain sequences AD246594-
 CC AD246598, and respectively inserting these 5 DNA fragments into genome of
 CC HSV by applying genetic engineering to give the recombinant HSV, large-
 CC scale production of 5 serotype recombinant adeno-associated viruses (AAV)
 CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-
 CC strain vector cell i.e. recombinant AAV vector cell-line, infecting the
 CC corresponding vector cell-line with the 5 recombinant HSV, producing
 CC recombinant AAV under the infective effect of the 5 recombinant HSV in
 CC the vector cell-line, separating and purifying the 5 serotype recombinant
 CC AAV after lysing the AAV-containing cells and culture liquor to give a
 CC crude lysate and further purification of rAAV by density-gradient
 CC centrifugation or affinity chromatography) and a recombinant vector
 CC plasmid pSNAV-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV
 CC -5 or AAV-6 genome, with immediate-early enhancer and promoter of
 CC cytomegalovirus, and a polyclonal site and a polyA signal, respectively,
 CC between the ITR (inverted terminal repeat), and neomycin-resistance gene-
 CC expressing cassette at outer edge of ITR). The DNA sequence is inserted
 CC into XbaI site in UI2 or UI44 gene in HSV genome. The DNA sequence of
 CC sequence AD246594-AD246598 can also be inserted into other non-essential
 CC gene regions in HSV genome. The recombinant HSV is optionally inserted
 CC with other DNA sequences homologous with the already-specified fragments.
 CC The vectors are for use in gene therapy of e.g. cancer, respiratory
 CC diseases and neural diseases. The virus vectors are safe, with long
 CC expression time and wide-spectrum of cell infection, even non-cleaved
 CC cells and reverse axonal conduction through the incorporated HSV vectors,
 CC and high transfer efficiently. The present sequence is the HSV-AAV
 CC sequence repcap6 for the AAV/HSV vectors of the invention.
 XX
 SQ Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;
 Query Match 81.8%; Score 3831.4; DB 14; Length 4239;
 Best Local Similarity 94.3%; Pred. No. 0;
 Matches 3997; Conservative 0; Mismatches 236; Indels 4; Gaps 2;

Db 306 GAAGTCGACGCGCATTTCTTGACGGAATGGCGCCGTGTGAGTAAGCCCGGAGGCCCT 365
 Qy 550 CTTCTTTGTTCAAGTTCCAGAAAGGCGAGCTCTACTTCCACTCCATATTCTGTGGAGAC 609
 Db 366 TTTCTTTGTGCAATTTTGGAAGGAGAGAGCTACTTCCATGACGCGCTCGGGAAC 425
 Qy 610 CACGGGGTCAAAATCCATGTGTGTGGGCGCTTCTCTGAGTGAATTAACGACAAGCTGT 669
 Db 426 CACGGGGTGAATTCATGTGTTTGGAGCTTTTCTGAGTCAAGATTCGCAAAAATGAT 485
 Qy 670 GCAGACATCTACCGCGGGATCGAGCGGACCTCCCACTGTGTTCCGGTGAACCAAGAC 729
 Db 486 TCAGGAAATTTACCGCGGGATCGAGCGGACCTTTCGCAAACTGTGTTCCGGTGAACCAAGAC 545
 Qy 730 GCGTAATGGCCCGGAGGGGGGAACAGGTGTGAGAGAGTGTCTATCCCACTACT 789
 Db 546 CAGAAATGGCCCGGAGGGGGGAACAGGTGTGAGAGAGTGTCTATCCCACTACT 605
 Qy 790 CCGGCCCAAGACTAGCCCGAGCTGACAGTGGCGGTGACTAATGAGAGATATATAG 849
 Db 606 GCTCCCAAAACCAAGCTTAGCTTCAAGTGGCGGTGACTAATGAGAGATATATAG 665
 Qy 850 GCGGTGTTAAACCTGGCCGAGCCAAACGCGCTGTGGCGGACGACCTGACCGTCA 909
 Db 666 GCGGTGTTGAATCTCAAGAGCGTAAACGTTGTGGCGGACGATCTGACGACGTGTC 725
 Qy 910 CCAAGCCAGAGACAAACAAAGGAATCTGAATCCCAATCTGAACGCGCTGTCAATCC 969
 Db 726 GCACACGAGAGAGACAAACAAAGGAATCTGAATCCCAATCTGTATGCGCGGTATCAG 785
 Qy 970 GTCAAAACCTCCGACGCTACATGAGAGCTGTGGGGGTGTGTGAGCCGGGACATCAC 1029
 Db 786 ATCAAAATCTTACGACGATGATGATGAGCTGTGGGGGTGTGTGAGCCGGGATCAC 845
 Qy 1030 CTCGAGAGAGAGATGATTCAGAGAGACAGGCTCTGTATCTCTTCAACGCGGCTTC 1089
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 Qy 1270 CCGCTGGGCGCAAAAGGTTCCGAAAACGCAACATCTGTGCTGTTTGGGCGGCGAC 1329
 Db 1086 GGAATGGGCGCAAAAGGTTCCGAAAACGCAACATCTGTGCTGTTTGGGCGGCGAC 1145
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Db 4203 GCACCCGTTACCTCACCCGCTCCCTGTAATGTTGTGT 4239

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RESULT 10
ADM39398
ID ADM39398 standard; DNA; 4347 BP.
XX
AC ADM39398;
XX
DT 24-MAR-2005 (first entry)
XX
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 1.
XX
KM genetically engineered microorganism; vector; rep; cap; ds.
XX
OS Adeno-associated virus 2.
OS Chimeric.
OS Unidentified.
XX
PN CN1461805-A.
XX
PD 17-DEC-2003.
XX
PF 27-MAY-2002; 2002CN-00117965.
XX
PR 27-MAY-2002; 2002CN-00117965.
XX
PA (BENNY-) BENYUAN ZHENG YANG GENETIC TECHNOLOGY CO.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2004-248658/24.

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XX Structure of a recombinant herpes simplex virus and its use.
PT
PS Claim 1; SEQ ID NO 1; 102bp; Chinese.
XX
CC The invention relates to a novel recombinant herpes simplex virus (rHSV)
CC whose genome is respectively inserted by the Adeno-associated virus (AAV)
CC rep gene and cap gene. The AAV genes may be derived from viruses AAV1,
CC AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
CC useful for generating recombinant vectors with high efficiency and no
CC need of reconfiguration. The current sequence is that of the Adeno-
CC associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
CC DNA (SEQ ID 1) of the invention.
XX
SQ Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;
Query Match 81.2%; Score 3802; DB 13; Length 4347;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;
Qy 191 GTCTGTTATTAAGGTCACTGATGTTTTCGACATTTTCGACACCATGTGTGACGC 250
Db 6 GTCTGTTATTAAGGTCACTGATGTTTTCGACATTTTCGACACCATGTGTGACGC 65
Qy 251 TGGGATTTTAAGCCGAGTGAAGCAGCAGAGGTCTCCATTTTGAAGCGGAGTTTGAACG 310
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Qy 550 CTTCCTTTGTTAGTTTCAAGAAAGGCGAGCTCTTCACTTCCATATTTCTGTGAGAC 609
Db 366 TTTCCTTTGTTAGTTTCAAGAAAGGCGAGCTCTTCACTTCCATGACGCTGTGGAAC 425
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    |||
Db 3303 GCCAAGCGCTGACCCGCGCTGATGAATCCTCTCATGACCAAGTACCTGTATTAACCTGAGACA 3362
OY 3550 GAACTCACCAATGATCCGGAAGTGGCCAAACAGAGGACTGTGTTTACCGTGGGCTC 3609
    |||
Db 3363 GAACTCACCAATGATCCGGAAGTGGCCAAACAGAGGACTGTGTTTACCGTGGGCTC 3422
OY 3610 CAGCTGGCATGTCTGTTGAGCCCAAAAAGTGGCTACCTGAGCCCTGTTACCGCGACAGC 3669
    |||
Db 3423 CAGCTGGCATGTCTGTTGAGCCCAAAAAGTGGCTACCTGAGCCCTGTTACCGCGACAGC 3482
OY 3670 GCGTTTCTTAAAAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 3729
    |||
Db 3483 GCGTTTCTTAAAAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 3542
OY 3730 AATTAACCTTAAATGGGGTGAATCTATTAATCAACCTGGGCACTGCTATGGGCTACACA 3789
    |||
Db 3543 AATTAACCTTAAATGGGGTGAATCTATTAATCAACCTGGGCACTGCTATGGGCTACACA 3602
OY 3790 AAGACGACAAAGACAAGTCTTTCATGAGCGGTGTCATGATGTTTGGAAAGAGAGCG 3849
    |||
Db 3603 AAGACGACGAGACAAAGTCTTTCATGAGCGGTGTCATGATGTTTGGAAAGAGAGCG 3662
OY 3850 CCGGAGCTTCAACAACCTGATTTGACAATGTATGATCAACAGACGAAAGAAATCAAG 3909
    |||
Db 3663 CCGGAGCTTCAACAACCTGATTTGACAATGTATGATTTACAGACGAAAGAAATTAAG 3722
OY 3910 CCACCTAACCCCGTGGCCACCCGAAAGATTTGGGACGTGTCAGTCAATCTCCAGACAGACA 3969
    |||
Db 3723 CCACCTAACCCCGTGGCCACCCGAAAGATTTGGGACGTGTCAGTCAATCTCCAGACAGACA 3782
OY 3970 GCACAGACCTGTCGACCCGAGATGTGATGTTATGGAGCCTTACCTGAAATGTTGTC 4029
    |||
Db 3783 GCACAGACCTGTCGACCCGAGATGTGATGTTATGGAGCATTACTGGCAATGTTGTC 3842
OY 4030 AAGACGAGAGGTATTAACCTGCAAGGCTCTAATTTGGGCCAAAATTCCTCAACAGATGAC 4089
    |||
Db 3843 AAGATAGAGAGGTATTAACCTGCAAGGCTCTAATTTGGGCCAAAATTCCTCAACAGATGAC 3902
OY 4090 ACTTTCACCCGCTCTCTCAATGGGCGGCTTGGACCTTAAGACCCGCTCTCTGAGATC 4149
    |||
Db 3903 ACTTTCACCCGCTCTCTCAATGGGCGGCTTGGACCTTAAGAAACCCGCTCTCTGAGATC 3962
OY 4150 TCATCAAAAAACAGCGCTCTCTGCGAATTCCTCCGCGAGAGTTTTCGCGTCAAAAGTTG 4209
    |||
Db 3963 TCATCAAAAAACAGCGCTCTCTGCGAATTCCTCCGCGAGAGTTTTCGCGTCAAAAGTTG 4022
OY 4210 CTTCAATTATCAACCAAGTATTCACAGACAAAGTACGCTGAGATTGAATGGAGCTTC 4269
    |||
Db 4023 CTTCAATTATCAACCAAGTATTCACAGACAAAGTACGCTGAGATTGAATGGAGCTTC 4082

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OY 4270 AGAAGAAAAACGAAACGCTGGAAATCCGGAAGTGCAGATATCATCTAATGCAAAAT 4329
    |||
Db 4083 AGAAGAAAAACGAAACGCTGGAAATCCGGAAGTGCAGATATCATCTAATGCAAAAT 4142
OY 4330 CTGCCAACGTTGATTTCACTGTCGACAAACAATGACCTTATTAATGAGCTGCCCCATG 4389
    |||
Db 4143 CTGCCAACGTTGATTTCACTGTCGACAAACAATGACCTTATTAATGAGCTGCCCCATG 4202
OY 4390 GACCCGTTAATCTCAACCCGTCCTGTAATGTGTATTAATTAATTAATTAATTAATTCG 4449
    |||
Db 4203 GACCCGTTAATCTCAACCCGTCCTGTAATGTGTATTAATTAATTAATTAATTAATTCG 4262
OY 4450 TGTGAGTTGAATGTTGTCATGTCCTTATTAATTAATTAATTAATTAATTAATTAATTCG 4509
    |||
Db 4263 TTTGAGTTGAATGTTGTCATGTCCTTATTAATTAATTAATTAATTAATTAATTAATTCG 4321
OY 4510 TACACATTAACTGCTTAAGTTGGCTT 4535
    |||
Db 4322 TACACATTAACTGCTTAAGTTGGCTT 4347

RESULT 11
AD246594
ID AD246594 standard; DNA; 4347 BP.
XX
AC AD246594;
XX
DT 30-JUN-2005 (first entry)
XX
DE HSV-AAV sequence rep2cap1 for AAV/HSV vectors.
XX
KM Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic;
XX respiratory disease; respiratory-gen.; neurological disease;
XX neuroprotective; ds.
XX
OS Adeno-associated virus.
XX
PN Human herpesvirus 1.
XX
PD WO2005035743-A1.
XX
21-APR-2005.
XX
15-OCT-2003; 2003WO-CN000861.
XX
15-OCT-2003; 2003WO-CN000861.
XX
(PATC-) AGTC GENE TECHNOLOGY CO LTD.
XX
Mu X, Cao H, Dong X;
XX
WPI; 2005-296279/30.
XX
PT large-scale production, isolation and purification of serotype adeno-
XX associated virus vectors by infecting cells with recombinant herpes
XX simplex virus vectors, for use in gene therapy of e.g. cancer and
XX respiratory diseases.
XX
PS Claim 1; SEQ ID NO 1; 79pp; Chinese.
XX
XX
CC The invention relates to a recombinant herpes simplex virus (HSV)
CC characterized in that its genome is inserted with a DNA sequence selected
CC from nucleotide sequences of AD246594-AD246598 or their homologous
CC sequences. Also included are preparing the recombinant HSV (comprising
CC the construction of DNA fragments that contains sequences AD246594-
CC AD246598, and respectively inserting these 5 DNA fragments into genome of
CC HSV by applying genetic engineering to give the recombinant HSV), large-
CC scale production of 5 serotype recombinant adeno-associated viruses (AAV)
CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-
CC strain vector cell i.e. recombinant AAV vector cell-line, infecting the
CC corresponding vector cell-line with the 5 recombinant HSV, producing
CC recombinant AAV under the infective effect of the 5 recombinant HSV in
CC the vector cell-line, separating and purifying the 5 serotype recombinant
CC AAV after lysing the AAV-containing cells and culture liquor to give a

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crude lysate and further purification of rAAV by density-gradient centrifugation or affinity chromatography) and a recombinant vector plasmid pSNV-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV-5 or AAV-6 genome, with immediate-early enhancer and promoter of cytomegalovirus, and a polyclonal site and a polyA signal, respectively, between the ITR (inverted terminal repeat), and neomycin-resistance gene-expressing cassette at outer edge of ITR). The DNA sequence is inserted into XbaI site in U2 or U44 gene in HSV genome. The DNA sequence of sequence AD246594-AD246598 can also be inserted into other non-essential gene regions in HSV genome. The recombinant HSV is optionally inserted with other DNA sequences homologous with the already-specified fragments. The vectors are for use in gene therapy of e.g. cancer, respiratory diseases and neural diseases. The virus vectors are safe, with long expression time and wide-spectrum of cell infection, even non-cleaved cells and reverse axonal conduction through the incorporated HSV vectors, and high transfer efficiently. The present sequence is the HSV-AAV sequence repCap1 for the AAV/HSV vectors of the invention.

Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

Query Match 81.2%; Score 3802; DB 14; Length 4347;

Best Local Similarity 92.6%; Pred. No. 0; Mismatches 315; Indels 5; Gaps 3;

Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;

Qy 191 GTCTGATTTAGAGTCACTGATGTTTTCGACATTTTCGACACCATGTGTACGC 250
Db 6 GTCTGATTTAGAGTCACTGATGTTTTCGACATTTTCGACACCATGTGTACGC 65
Qy 251 TGGGATTTTAAAGCCGAGTGCACGACGGGTCTTCATTTTGAAGCCGGAGTTGAACG 310
Db 66 TGGGATTTTAAAGCCGAGTGCACGACGGGTCTTCATTTTGAAGCCGGAGTTGAACG 125
Qy 311 CGCAG-CGSCATGCGGGGGTTTACGAGATTGTATTAAGTCCCGACGACCTTGAACA 369
Db 126 CGCAGCGCCATGCGGGGGTTTACGAGATTGTATTAAGTCCCGACGACCTTGAACG 185
Qy 370 GCATCTGCGCGGCAATTTCTGACAGCTTTGTAACTGGGTGCGGAGAAAGATGGAGTT 429
Db 186 GCATCTGCGCGGCAATTTCTGACAGCTTTGTAACTGGGTGCGGAGAAAGATGGAGTT 245
Qy 430 GCGCCGACATTTCTGACATGATCTGAATCTGAATTGAGAGGACCCCTGACCGTGGCGA 489
Db 246 GCGCCGACATTTCTGACATGATCTGAATCTGAATTGAGAGGACCCCTGACCGTGGCGA 305
Qy 490 GAAGCTGACGCGGCACTTCTGATCTCACTGGGCGCGTGAAGTAAAGCCCGAGAGCCCT 549
Db 306 GAAGCTGACGCGGCACTTCTGATCTCACTGGGCGCGTGAAGTAAAGCCCGAGAGCCCT 365
Qy 550 CTCTCTTTGTCAGTTGAGAAAGGCGAGTCTTCACTTCCACTTCATATTTGTGAGAC 609
Db 366 TTTCTTTGTCAGTTGAGAAAGGCGAGTCTTCACTTCCACTTCATATTTGTGAGAC 425
Qy 610 CACGGGGTCAAAATTCATGTGTGTGGCGGCTTCTGATGTCAGATTAGCGACAAGCTGCT 669
Db 426 CACGGGGTCAAAATTCATGTGTGTGGCGGCTTCTGATGTCAGATTAGCGACAAGCTGCT 485
Qy 670 GCAGACCATCTACGCGGGGATTCAGACCGACCTCGCCCACTGTTGCGGTGACCAAGAC 729
Db 486 TCAGAGAAATTTACGCGGGGATTCAGACCGACCTTTCGCAAACTGGTTCCGGGTCACAAAGAC 545
Qy 730 GCGTAATGCGCGGAGGGGGAACAAGGTGTGAGCGAGTCTACATCCCACTACT 789
Db 546 CAGAAATGCGCGGAGGGGGAACAAGGTGTGAGCGAGTCTACATCCCACTACT 605
Qy 790 CTTGCCCCAAGCTACGCCCCGAGTGTGAGTGGCGGTGACTAACTAGAGAGTATATAG 849
Db 606 GCTCCCCAAGCCAGCTGAGCTTCAAGTGGCGGTGACTAACTAGAGAGTATATAG 665
Qy 850 CGCGTGTTTAAACCTGCGCGGCAACGCGCTCGTGGCGACGACCTGACCCAGCTGAG 909
Db 666 CGCGTGTTTAAACCTGCGCGGCAACGCGCTCGTGGCGACGACCTGACCCAGCTGAG 725
Qy 910 CCAAGCCCAAGAGCAAAAGAGATCTGAACCCCAATTCTGACGCGCTGTCTATCG 969

Db 726 GCAGACCCAGAGCAGAAACAAGAGATCTCAAAATCCCAATTCGATGCGCGGTGATCAG 785
Qy 970 GTCAAAAACCTCCGACGCTCAATGAGCTGTGCGGGTGTGTGACCGGGGCATCAC 1029
Db 786 ATCAAAAACCTCCGACGCTCAATGAGCTGTGCGGGTGTGTGACCGGGGCATCAC 845
Qy 1030 CTCGGAAGAGAGTGAATCCAGAGAGACAGGCTCTGATATCTCTTCAACGCGCTC 1089
Db 846 CTCGGAAGAGAGTGAATCCAGAGAGACAGGCTCTGATATCTCTTCAATGCGGCTC 905
Qy 1090 CAACTCGCGGTCCGATCAAGCGCGCTTGAACATGTCGCGAAGTCAATGCGCTGAC 1149
Db 906 CAACTCGCGGTCCGATCAAGCGCGCTTGAACATGTCGCGAAGTCAATGCGCTGAC 965
Qy 1150 CAAATCCGCGCGCATCACTGTGAGGCCCCGCTCCGCGCGGACATTAACCAACCG 1209
Db 966 TAAACCGCGCGCATCACTGTGAGGCCCCGCTCCGCGCGGACATTAACCAACCG 1025
Qy 1210 CATTACCGCATCTGAGCTGAACGCGCTACGACCTGCTACGCGCGCTCTCTTCT 1269
Db 1026 GATTATTAATTTTGAATCAAAAGGCTAGATCCCAATATGCGGCTTCCGCTTCT 1085
Qy 1270 CGGCTGGCCGAGAAAAGTTTGGAAAACCAACATCTGCTGTTGGCGCGCAC 1329
Db 1086 GGGATGGGCGACGAAAAGTTTGGAAAACCAACATCTGCTGTTGGCGCGCAC 1145
Qy 1330 CAGGGGCAAGCAACATCCGGAAGCATGCGCCACGCGGTGCTTCAAGCGCTCGT 1389
Db 1146 TACGGGAAGCAACATCCGGAAGCATGCGCCACATGCTGCTTCAAGCGCTCGT 1205
Qy 1390 CAATGAGCAATGAGATCTTCTCTTCAAGATGCGTGAAGATGATCTGAT 1449
Db 1206 AAATGAGCAATGAGATCTTCTCTTCAAGATGCGTGAAGATGATCTGAT 1265
Qy 1450 GGAAGAGGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCAATTTCCGCGGAC 1509
Db 1266 GGAAGAGGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCAATTTCCGCGGAC 1325
Qy 1510 CAAGTGGCGGTGACCAAAAAGTGCAGATGCTCGGCCAGATGATCCACCCCGGAT 1569
Db 1326 CAAGTGGCGGTGACCAAAAAGTGCAGATGCTCGGCCAGATGATCCACCCCGGAT 1385
Qy 1570 CGTCACCTCCAAACAACAATGTGCGCGGTGATTTGAGGGAACGACACCTTGAACA 1629
Db 1386 CGTCACCTCCAAACAACAATGTGCGCGGTGATTTGAGGGAACGACACCTTGAACA 1445
Qy 1630 CCAAGACCGCTTGCAGAGACGAGATGTTCAATTTGAATCAACCGCGCTTGAAGATGA 1689
Db 1446 CCAAGACCGCTTGCAGAGACGAGATGTTCAATTTGAATCAACCGCGCTTGAAGATGA 1505
Qy 1690 CTTTGGCAAGTGACAAAAGCAGAAATCTTCCGCTGGCGGACGATCACT 1749
Db 1506 CTTTGGCAAGTGACAAAAGCAGAAATCTTCCGCTGGCGGACGATCACT 1565
Qy 1750 GACCGAGTGGCGGATGATTTTCACTGAGAAAAGGTGAGCCAAACAACGACCCGCCC 1809
Db 1566 GATTGAGTGGAGATGATTTTCACTGAGAAAAGGTGAGCCAAACAACGACCCGCCC 1625
Qy 1810 CGATGACCGCGATTAAGGCAAGCCCAAGCGGCTGCTCACTGCGGATTCATGAC 1869
Db 1626 CAGTGAAGCAGATTAAGGCAAGCCCAAGCGGCTGCTCACTGCGGATTCATGAC 1685
Qy 1870 GTCAGACGCGGAAGGAGCTCGGATGCTTTCGCAAGGATCCAAACAATGTTCTCG 1929
Db 1686 GTCAGACGCGGAAGGAGCTCGGATGCTTTCGCAAGGATCCAAACAATGTTCTCG 1742
Qy 1930 TCAAGCGGAGATGCTTCAAGTGTGTTTCCCTGCAAAACATGCGAGAAATGAATCAAA 1989
Db 1743 TCAAGCGGAGATGCTTCAAGTGTGTTTCCCTGCAAAACATGCGAGAAATGAATCAAA 1802
Qy 1990 TTTCAATTTTCTTCAAGCAGGAGACAGAGATCTTCAAGATGTTTCCCGGCGGTGC 2049

Db	1803	TTTCAACATTTCCTTCACGACACGGGACGAGAACCTGTTCCAGATGCTTCCCGCGCTGTC	1862
Qy	2050	AGAAATCTCAACCGGCTGTCAGAAAGAGGACGTATCGAAACCTCTGTGCATTCATCATCT	2109
Db	1863	AGAAATCTCAACCGGCTGTCAGAAAGAGGACGTATCGAAACCTCTGTGCATTCATCATCT	1922
Qy	2110	GCTGGGGGGGGCTCCCGAGATTGCTTGGCTCGGCTTCGCATCTGGTCAACGTGGATCTGGA	2165
Db	1923	GCTGGGGGGGGCTCCCGAGATTGCTTGGCTCGGCTTCGCATCTGGTCAACGTGGACCTGGA	1982
Qy	2170	TGACGTGTGTTCTGAGCAATTAATGACTTAAACCAAGTATGCGCTCCGATGGTTATCTTC	2229
Db	1983	TGACTGTGTTCTGAGCAATTAATGACTTAAACCAAGTATGCGCTCCGATGGTTATCTTC	2042
Qy	2230	CAGATTGGCTCGAGAGCAACCTCTCTGAGGGCAATTGGCAGAGTGCGGACCTTGAAACCTG	2289
Db	2043	CAGATTGGCTCGAGAGCAACCTCTCTGAGGGCAATTGGCAGAGTGCGGACCTTGAAACCTG	2102
Qy	2290	GAGCCCCGAAACCCAAAGCCAAACGACAAAGACGAGACGAGCCGGGGTCTGGTCTTC	2349
Db	2103	GAGCCCCGAAAGCCAAACCCAAACGACAAAGACGAGACGAGCCGGGGTCTGGGCTTC	2162
Qy	2350	CTGGGTACAAGTACCTCGGACCCCTTCAACGACTGTGACAAAGGGGAGGCCCTGCAACGGG	2409
Db	2163	CTGGGTACAAGTACCTCGGACCCCTTCAACGACTGTGACAAAGGGGAGGCCCTGCAACGGG	2222
Qy	2410	CGGATGACAGCGGCCTCGAGCACGACAAAGCCCTACGACACAGAGTCAAAACGGGTGACA	2469
Db	2223	CGGAGCGACGCGGCCCTCGAGCACGACAAAGCCCTACGACACAGAGTCAAAACGGGTGACA	2282
Qy	2470	ATCGGTACCTGCGGTATTAACAACGCGCGACGCGGAGTTTCAGAGCGTCTGCAAGAGATA	2529
Db	2283	ATCGGTACCTGCGGTATTAACAACGCGCGACGCGGAGTTTCAGAGCGGTCTGCAAGAGATA	2342
Qy	2530	CGTCTTTTGGGGGGCAACTCGGGCGAGACAGTCTTCAGGCCCAAGAAAGGTTCTCGAAC	2589
Db	2343	CGTCTTTTGGGGGGCAACTCGGGCGAGACAGTCTTCAGGCCCAAGAAAGGGGTTCTCGAAC	2402
Qy	2590	CTTTTGGCTGTGAGGAGAGGTGTGTAGAAGGCTCTGGAAGAAAGCTCGCGGTAGAGC	2649
Db	2403	CTTCTGGTCTGGTTGAGGAAAGCGCTTAAGACGGCTCTCGAAAGAAAGTCCGGTAGAGC	2462
Qy	2650	AGTGGCCACAAGAGCCAGACTCTCTCGGGCATTTGGCAAGACAGGCCAGAGCCCGCTA	2709
Db	2463	AGTGGCCACAAGAGCCAGACTCTCTCGGGCATTTGGCAAGACAGGCCAGAGCCCGCTA	2522
Qy	2710	AAAAGAGCTCAATTTTGGTGAAGCTGGCGACTCAGAGTCAAGTCCCGACCAACACTC	2769
Db	2523	AAAAGAGCTCAATTTTGGTGAAGCTGGCGACTCAGAGTCAAGTCCCGACCAACACTC	2582
Qy	2770	TGGGGAACCTCCAGCAACCCCCGTGTGTGGGACCTTAACATATGGCTTCAGGCCGTG	2829
Db	2583	TGGGGAACCTCCAGCAACCCCCGTGTGTGGGACCTTAACATATGGCTTCAGGCCGTG	2642
Qy	2830	GCGCACCAATGGCAGACAATACGAAAGGCGCGACGAGTGGGTATATGCTCAGAAATTT	2889
Db	2643	GCGCACCAATGGCAGACAATACGAAAGGCGCGACGAGTGGGTATATGCTCAGAAATTT	2702
Qy	2890	GGCATTTGCATTTCCATATGCTGGGCGACAGAGTATATCAACCAAGCAACCCGAACATGG	2949
Db	2703	GGCATTTGCATTTCCATATGCTGGGCGACAGAGTATATCAACCAAGCAACCCGAACATGG	2762
Qy	2950	CCTTGCCCACTATATACAAACCAACCTTAACAGCAAAATTCAGATGCTTCAACGGGGCCA	3009
Db	2763	CCTTGCCCACTATATACAAACCAACCTTAACAGCAAAATTCAGATGCTTCAACGGGGCCA	2822
Qy	3010	GCAACGACCAACCACTATTTGGCTTACAGCAACCCCTGGGGGTATTTGATTTCAACAGAT	3069
Db	2823	GCAACGACCAACCACTATTTGGGCTTACAGCAACCCCTGGGGGTATTTGATTTCAACAGAT	2882
Qy	3070	TTCACATGCGCAATTTCTCACACAGTGACTGGCAGCACTCATATCAACACAAATTTGGGATTC	3129
Db	2883	TTCACATGCGCAATTTTTCACACAGTGACTGGCAGCACTCATATCAACAAATTTGGGATTC	2942

QY	3130	GGCCCCAAGAGACTCACTTCAAGCTCTTTCACATCCAGTCAAGAGGTCAAGACGATG	3189
Db	2943	GGCCCAAGAGACTCACTTCAAACTCTTTCACATCCAAAGAGGTCAAGACGATG	30020
QY	3190	ATGGCGTCAAGCAATCCGTATATACTTACAGCAGCGGTTCAAGTCTTTCGACTCG	3249
Db	3003	ATGGCGTCAACACATCCGTATATACTTACAGCAGCGGTTCAAGTCTTTCGACTCG	30632
QY	3250	AGTACCAAGTCCCGTACGTCTCGGCTCTGGGCACAGGGCTGCTCCCTCCGTTCCCG	3309
Db	3063	AGTACCAAGTCCCGTACGTCTCGGCTCTGGGCACAGGGCTGCTCCCTCCGTTCCCG	31222
QY	3310	CGGAGGTGTCAATGATTCGGAGTACCGGCTACTAAGCTCAACAAATGGACGACGAG	3369
Db	3123	CGGAGGTGTCAATGATTCGGAGTACCGGCTACTAAGCTCAACAAATGGACGACGAG	31822
QY	3370	TGGAGCGTCACTCTTTTACTGCTCGTAATATTTCCATTCGAGATGCTGAAACGGGCA	3429
Db	3183	TGGAGCGTCACTCTTTTACTGCTCGTAATATTTCCATTCGAGATGCTGAAACGGGCA	32422
QY	3430	ATTAATTTAATCTTTCAGCTACACCTTTCGAGACGTGCTTTTCCACAGCAGCTACCGGCACA	3489
Db	3243	ACAAATTTAATCTTTCAGCTACACCTTTCGAGAGGTCTTTTCCACAGCAGCTACCGGCACA	33020
QY	3490	GGCAGAGCTGGACCGGCTGATGAACTCTTCATCGACCACTATCTGTATTAACCTGAACA	3549
Db	3303	GGCAGAGCTGGACCGGCTGATGAACTCTTCATCGACCACTATCTGTATTAACCTGAACA	33632
QY	3550	GAATCTCAACATCAGTCGCGAAGTCCCAAAACAAGACTTGCTGTTTACCGCTGGTCTC	3609
Db	3363	GAATCTCAACAAATCAGTCGCGAAGTCCCAAAACAAGACTTGCTGTTTACCGCTGGTCTC	34222
QY	3610	CAGCTGGCATGCTGTTCAGCCCAAAAATGAGTACCTGGACCGCTTTACCGGACGAGC	3669
Db	3423	CAGCTGGCATGCTGTTCAGCCCAAAAATGAGTACCTGGACCGCTTTATGGCAGCAGC	34822
QY	3670	GGGTTTCTAAAACAAAAACAGACAACAACAAGCAACTTTACCTGACCTGCTGTTCAA	3729
Db	3483	GGGTTTCTAAAACAAAAACAGACAACAACAAGCAACTTTACCTGACCTGCTGTTCAA	35422
QY	3730	AATATAACCTTAATGGGCGTGAATCTTAATCAACCCTGGACCTGCTATGGCTTCACCA	3789
Db	3543	AATATAACCTTAATGGGCGTGAATCTTAATCAACCCTGGACCTGCTATGGCTTCACCA	36020
QY	3790	AAGAAGCAAAAGACAAGTTCTTTCCCATGAGCGGGTGCATGATTTTGGAAAGAGAGCG	3849
Db	3603	AAGAAGCAAGAAAGACAAGTTCTTTCCCATGAGCGGGTGCATGATTTTGGAAAGAGAGCG	36632
QY	3850	CCGGAGCTTCAAAACATGCAATTGGACAATGTCAATGATCAGACGAAAGGAAATCAAG	3909
Db	3663	CCGGAGCTTCAAAACATGCAATTGGACAATGTCAATGATCAGACGAAAGGAAATTTAAAG	37222
QY	3910	CCACTAACCCCGGTGGCCACCGAAGAATTTGGGACGTGGGAGCTCAATCTCCAGAGCACA	3969
Db	3723	CCACTAACCCCGGTGGCCACCGAAGAATTTGGGACCGTGGAGCTCAATTTCCAGAGCACA	37822
QY	3970	GCACAGACCTCTGCACCGGAGATGTGCATGTTATGGAGGCTTACCTTGATGATGTTGGC	4029
Db	3783	GCACAGACCTCTGCACCGGAGATGTGCATGTTATGGAGGCTTACCTTGATGATGTTGGC	3842
QY	4030	AAGACAGAGAGTATACCTGCAAGGCTCTATTTTGGGCAAAATTCCTTCAACGGAATGGAC	4089
Db	3843	AAGATAGAGAGCTGTAACCTGCAAGGCTCCATTTTGGGCAAAATTCCTTCAACAGATGGAC	39020
QY	4090	ACTTTCAACCCCTCTCTCTCAATGGGCGGCTTTGGACTTTAAGCACCCGCTCTCAGATCC	4149
Db	3903	ACTTTCAACCCGCTCTCTCTTAATGGGCGGCTTTGGACTTCAAGAACCCGCTCTCAGATCC	3962
QY	4150	TCATCAAAAAACAGCGCTGTTCTCTGCGAATCTCTCGGACAGAGTTTGGGCTAACAAAGTTTG	4209
Db	3963	TCATCAAAAAACAGCGCTGTTCTCTGCGAATCTCTCGGAGGAGTTTTCAGCTAACAAAGTTTG	4022

QY 4210 CTTGATTCATCAGCCAGTATTCCACAGACAAGTGAAGCTGAGATTGAATGAGAGCTGC 4269
DB 4223 CTTGATTCATCAGCCAGTATTCCACAGACAAGTGAAGCTGAGATTGAATGAGAGCTGC 4082
QY 4270 AGAAGAGAAACAGCAAAACGCTGGAATCCGGAAGTCACTATACATCTAATGCAAAAT 4329
DB 4083 AGAAGAGAAACAGCAAAACGCTGGAATCCGGAAGTCACTATACATCTAATGCAAAAT 4142
QY 4330 CTGCAACGTTGATTTGCTGAGCAACATGACCTTATAGAGCTGCGCCCAATG 4389
DB 4143 CTGCAACGTTGATTTGCTGAGCAACATGACCTTATAGAGCTGCGCCCAATG 4202
QY 4390 GCACCCGTTACCTGACCCGCTGCTGATTTGTTGTTAATCAATCAACCGGTTAATTCG 4449
DB 4203 GCACCCGTTACCTGACCCGCTGCTGATTTGTTGTTAATCAATCAACCGGTTAATTCG 4262
QY 4450 TGTGAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGTCACCATAGCAACGGT 4509
DB 4263 TTTGAGTTGAACTTTGGTCTCTGCTCTTATCTTATCTTATC-GGTTACCATGTTATAGCT 4321
QY 4510 TACACATTAAGCTGCTAGTGGGCTT 4535
DB 4322 TACACATTAAGCTGCTAGTGGGCTT 4347

RESULT 12

AEF81093
ID AEF81093 standard; DNA; 4347 BP.

AC AEF81093;

DT 06-APR-2006 (first entry)

DE Adeno-associated virus related rep2cap1 DNA SEQ ID NO 1.

KW growth; food; meat; rep2cap1; ds.

OS Adeno-associated virus.

PN CN162652-A.

PD 15-JUN-2005.

PF 08-DEC-2003; 2003CN-01117208.

PR 08-DEC-2003; 2003CN-01117208.

PA (ZHEN-) ZHENGYANG GENE TECH CO LTD BENYUAN.

PI Dong X;

DR WPI; 2005-749951/77.

PT Method for accelerating quick growth of animals and method for improving
PT quality of meat.

PS Disclosure; SEQ ID NO 1; 28bp; Chinese.

CC The invention relates to a method for promoting fast growth of animal and
CC improving its meat quality features that the adenovirus associated virus
CC carrier, especially the type-A one, is introduced to the growth hormone
CC gene or relative gene. The present sequence represents an adeno-
CC associated virus related rep2cap1 DNA.

XX Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

Query Match 81.2%; Score 3802; DB 14; Length 4347;

Best Local Similarity 92.6%; Pred. No. 0;
Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;

QY 191 GTCTGATTTAGAGTCACTGAGTGTGTTTGGCAGATTTTGGCAGACCATATGTCACGC 250
DB 6 GTCTGATTTAGAGTCACTGAGTGTGTTTGGCAGATTTTGGCAGACCATATGTCACGC 65

QY 251 TGGGATTTTAAGCCCGAGTGAGCAGCGAGGGTCTCCATTTTGAAGCGGAGTTTGAACG 310
DB 66 TGGGATTTTAAGCCCGAGTGAGCAGCGAGGGTCTCCATTTTGAAGCGGAGTTTGAACG 125
QY 311 CGCAG-CGCCATGCGGGGGTTTTTACGAGATTGATTTAAGTCCCGACGCACTTGACGA 369
DB 126 CGCAGCGCCGATCGGGGGTTTTTACGAGATTGATTTAAGTCCCGACGCACTTGACG 185
QY 370 GCATCTGCGCGGATTTCTGACAGCTTTTGAACTGGGAGCGGAGAGGATGGGAGTT 429
DB 186 GCATCTGCGCGGATTTCTGACAGCTTTTGAACTGGGAGCGGAGAGGATGGGAGTT 245
QY 430 GCGCCAGATTTGACATGATCTGATCTGATTTGAGCAGGCAACCCCTGACCGTGGCGGA 489
DB 246 GCGCCAGATTTGACATGATCTGATCTGATTTGAGCAGGCAACCCCTGACCGTGGCGGA 305
QY 490 GAAGCTGACCGGACTTCTTGCTGCACTGGCGCGCGTGAAGTAAAGGCGCGGAGGCTT 549
DB 306 GAAGCTGACCGGACTTCTTGCTGCACTGGCGCGCGTGAAGGCGCGGAGGCGCTT 365
QY 550 CTTCCTTTGTCAGTTGAGAAAGGGCGAGTCTTCCACCTGCATATTCGTGGAGAGC 609
DB 366 TTTCTTTTGTCAATTTGAGAAAGGGCGAGTCTTCCACATGCAAGTCTGTTGAGAAC 425
QY 610 CACGGGGGTCAAAATCCATGCTGCGCGCTTCTGAGTCAAGATTAGCAGCAAGCTGCT 669
DB 426 CACCGGGGTCAAAATCCATGCTTGTGGAGCGTTTCTGAGTCAAGATTAGCAGCAAGCTG 485
QY 670 GCAGACCATTTACCGCGGGATCCAGCCGACCTTGCCCACTGGTTGGCGGTACCAAGAC 729
DB 486 TCAGAGAAATTTACCGCGGGATCCAGCCGACCTTGCCCACTGGTTGGCGGTACCAAGAC 545
QY 730 GCGTAATGSGGCGGAGGGGGGAAACAAGTGTGAGAGAGTGTACATCCCAACTACT 789
DB 546 CAGAAATGSGGCGGAGGGGGGAAACAAGTGTGAGAGAGTGTACATCCCAACTACT 605
QY 790 CTTGCCAAGACTCAGCCCGAGCTGCACTGGGGGTGACTTAATGAGAGGATATTAAG 849
DB 606 CTTGCCAAGACTCAGCCCGAGCTGCACTGGGGGTGACTTAATGAGAGGATATTAAG 665
QY 850 CGCGTGTTTAACTTGCGCGCAAGCGGCTGCTGTCGCGCAAGACTTGACCAAGCTCAG 909
DB 666 CGCGTGTTTAACTTGCGCGCAAGCGGCTGCTGTCGCGCAAGACTTGACCAAGCTCAG 725
QY 910 CCAAGCCAGAGAGAGAAAGAGGAAATCGAATCCCAATTCAGCGCGCTGATCCG 969
DB 726 CCAAGCCAGAGAGAGAAAGAGGAAATCGAATCCCAATTCAGCGCGCTGATCCG 785
QY 970 GTCAAAAACCTCCGCAAGCTACAGTGAAGTGTGCGGGTGGCTGAGACCGGGGATCAC 1029
DB 786 ATCAAAAACCTCCGCAAGCTACAGTGAAGTGTGCGGGTGGCTGAGACCGGGGATCAC 845
QY 1030 CTCCGAGAGAGAGTGAATCCAGAGACCAAGGCTCTGATCTCTTCAACCGCGCTC 1089
DB 846 CTCCGAGAGAGAGTGAATCCAGAGACCAAGGCTCTGATCTCTTCAACCGCGCTC 905
QY 1090 CAATCGCGGTCCAGATTCAGAGCGGCTGAGCAATGCGGGAAGTCAAGCGGCTGAC 1149
DB 906 CAATCGCGGTCCAGATTCAGAGCGGCTGAGCAATGCGGGAAGTCAAGCGGCTGAC 965
QY 1150 CAAATCCGCGCCGACTACTGTGAGGCTCCGCTCCGCGCGGACATTTAAACCAACCG 1209
DB 966 TAAACCGCGCCGACTACTGTGAGGCTCCGCTCCGCGCGGACATTTCAAGCAATCG 1025
QY 1210 CATTTACCGATCTGAGAGCTGAACGCTTGAACCTGCTAGCGCGGCTCTCTTCT 1269
DB 1026 GATTTAATAAATTTTGGAACTTAACCGGCTGATCCCAATTAAGCGGCTCTCTCTTCT 1085
QY 1270 CGGCTGGGCGCAGAAAGGTTGAGAAAGCAACACCATCTGGCTGTTTGGCGCGGAC 1329
DB 1086 GGGATGGGCGCAGAAAGGTTGAGAAAGCAACACCATCTGGCTGTTTGGCGGCTGCAAC 1145

QY 1330 CACGGCAAGACCAATCGCGGAGCCATCGCCACGCCGTGCCCTTCTACGGCTGCGT 1389
Db 1146 TACCGGAAAGACCAATCGCGGAGGCCATAGCCCACTGTGCCCTTCTACGGGTCGT 1205
QY 1390 CAACCTGACCAATGGAATTTCCCTTCAACGATTCGCTGCAAGATGCTGATCTGCTG 1449
Db 1206 AAACTGACCAATGGAATTTTCCCTTCAACGATGCTGCTGCAAGATGCTGATCTGCTG 1265
QY 1450 GGAGAGGGCAAGATGACCGGCAAGGTGCTGAGTCCGCAAGGCCATTCGCGCGGACG 1509
Db 1266 GGAGAGGGGGAAGATGACCGGCCAAGGTGCTGAGTGGCCAAAGCCATTCGCGGAGAG 1325
QY 1510 CAAGGTGCGCTGAGACCAAAAGTGCAAGTCGTCCGCCAGATCGATCCCAACCCCGTGAT 1569
Db 1326 CAAGGTGCGCTGAGACCAAAATGCAAGTCGTCCGCCAGATAGACCCGACTCCGCTGAT 1385
QY 1570 GGTCACTTCCCAACCAATATGCGCCGCTGATTTGACGGGAAACAGACCACTTGGAGA 1629
Db 1386 GGTCACTTCCCAACCAATATGCGCCGCTGATTTGACGGGAACTCAACGACCTTGGAA 1445
QY 1630 CCAGACGCGCTTGACAGACCGGATGTTCAATTTTGAATCACCCGCGCTGAGAGATGA 1689
Db 1446 CCAGACGCGCTTGACAGACCGGATGTTCAATTTTGAATCACCCGCGCTGAGATGA 1505
QY 1630 CTTTGGCAAGGTGACCAAGCAGAAAGTCAAGAGTCTTCCGCTGGCGCAGAGATCACGT 1749
Db 1506 CTTTGGCAAGGTGACCAAGCAGAAAGTCAAGAGTCTTCCGCTGGCGCAGAAAGATCACGT 1565
QY 1750 GACCAAGGTGCGCATGAGTTCTAGTCAAAAGGTGAGCCAAACACAGACCCGCCCC 1809
Db 1566 GGTTAAGGTGAGCAATGAAATTTAGTCAAAAAGGTGAGCCAAAGAAAGCCGCCCC 1625
QY 1810 CGATGACGCGGATTAAGAGGAGCCCAAGCGGGCGTGCCTCAGTCGGGGATCATCGAC 1869
Db 1626 CAGTACCGCATATTAAGTGAACCCAAACGGGTGGCGAGTCAAGTTGGCGACCCATCGAC 1685
QY 1870 GTACAGCCGGAAGAGCTCCGCTGAGACTTTGCCACAGTACCAAAACAATGTTCTCG 1929
Db 1686 GTCAAGCCGGA --- AGCTTGATCACTACGCAACAGATACCAAAACAATGTTCTCG 1742
QY 1930 TCACGCGGCGATGCTTCAAGATGCTGTTCCCTGCAAAAATGCGAAGATGATCAGAA 1989
Db 1743 TCACGCGGCGATGCTTCAAGATGCTGTTCCCTGCAAAAATGCGAAGATGATCAGAA 1802
QY 1990 TTTCAACATTTGCTTCAAGACCGGGAACAAGACATGTTCAAAATGTTCCCGGGGTGTC 2049
Db 1803 TTTCAACATTTGCTTCAAGACCGGGAACAAGACATGTTCAAGATGTTCCCGGGGTGTC 1862
QY 2050 AGAATCTCAACCGGTGCTCAGAAAGAGACGTATCGAAACTCTGTGCATTCATCATCT 2109
Db 1863 AGAATCTCAACCGGTGCTCAGAAAGAGACGTATCGAAACTCTGTGCATTCATCATCT 1922
QY 2110 GCTGGGGCGGCTCCGAGATGCTTGTGCTCGGCTGCGATCTGTCAAAGTGGATCTGGA 2169
Db 1923 GCTGGGGCGGCTCCGAGATGCTTGTGCTCGGCTGCGATCTGTCAAAGTGGATCTGGA 1982
QY 2170 TGAATGCTTTCTGAGCAATAAATGAATTAACAGAGATGCTGCTCCGATGCTTCTTC 2229
Db 1983 TGAATGCTTTCTGAGCAATAAATGAATTAACAGAGATGCTGCTCCGATGCTTCTTC 2042
QY 2230 CAGATGCTCGAGACAACCTCTGAGGGCATTCGCGAGTGTGGGACTTGAACCTG 2289
Db 2043 CAGATGCTCGAGACAACCTCTCTGAGGGCATTCGCGAGTGTGGGACTTGAACCTG 2102
QY 2290 GAGCCCGGAAACCCAAAGCCAAACGAGAAAGCAGAGACGCGCGGGGTCTGTGCTTC 2349
Db 2103 GAGCCCGGAAACCCAAAGCCAAACGAGAAAGCAGAGACGCGCGGGGTCTGTGCTTC 2162
QY 2350 CTGGCTAAGATACCTCGGACCTTCAACGAGCTGACAAAGGGGAGCCCTCAACGCGG 2409
Db 2163 CTGGCTAAGATACCTCGGACCTTCAACGAGCTGACAAAGGGGAGCCCTCAACGCGG 2222
QY 2410 CGGATGACGCGGCTCGAGACGACAAGGCTTACGACCAAGCTCAAAAGGGGTGACA 2469

Db 2223 CGGACGACGCGGCTTCGAGACGACAAGGCTTAAGACAGGAGCTCAAAAGGGGTGACA 2282
QY 2470 ATCCGTACTCGGTGATTAACAACGCGCGAGCGCGAATTTCAAGAGGCTTCGAAAGATTA 2529
Db 2283 ATCCGTACTCGGTGATTAACAACGCGCGAGCGCGAATTTCAAGAGGCTTCGAAAGATTA 2342
QY 2530 GGTCTTTTGGGGGCAACCTCGGGGCGAGAGTCTTTCAGAGCCAAAGAGAGGTTCTCGAAC 2589
Db 2343 GGTCTTTTGGGGGCAACCTCGGGGCGAGAGTCTTTCAGAGCCAAAGAGGAGGTTCTCGAAC 2402
QY 2590 CTTTGGTCTGTGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAAGTCCGATGAGC 2649
Db 2403 CTCTCGTGTGTTGAGGAAGGCGCTTAAGACGGCTCTTGAAAGAAAGTCCGATGAGC 2462
QY 2650 AGTCCGCAAGAGCACAATCTCTCTCGGGCATTTGGCAAGACAGGCCAGACCCGCTA 2709
Db 2463 AGTCCGCAAGAGCACAATCTCTCTCGGGCATTTGGCAAGACAGGCCAGACCCGCTA 2522
QY 2710 AAAAGAGACTAATTTTGTGAGACTGAGCTGAGTCAAGTCCCGAGCCACAACCTC 2769
Db 2523 AAAAGAGACTAATTTTGTGAGACTGAGCTGAGTCAAGTCCCGAGCTCAACACTTC 2582
QY 2770 TCGAGAACTTCAGCAACCCCGCTGCTGTGGACCTTACTTCAATGCTTCAAGCGGTG 2829
Db 2583 TCGAGAACTTCAGCAACCCCGCTGCTGTGGACCTTACTTCAATGCTTCAAGCGGTG 2642
QY 2830 GCGCACATGCGAGACAATAAGAGGCGCGAGAGTGGATTAATGCTCAGGAAATTT 2889
Db 2643 GCGCACATGCGAGACAATAAGAGGCGCGAGAGTGGATTAATGCTCAGGAAATTT 2702
QY 2890 GGCATTGGATTCCACATGCGGGGCGAGAGTCAATACACAGCAGCCGGAACATGG 2949
Db 2703 GGCATTGGATTCCACATGCGGGGCGAGAGTCAATACACAGCAGCCGGAACATGG 2762
QY 2950 CTTGCCCCACTTATTAACAACCACTCTTACAAGCAATCTCCAGTCTTCAACGGGGGCA 3009
Db 2763 CTTGCCCCACTTATTAACAACCACTCTTACAAGCAATCTCCAGTCTTCAACGGGGGCA 2822
QY 3010 GCAACGACACCACTACTTCCGCTTACAGACACCCCTGGGGGTATTTGATTTCAACAGAT 3069
Db 2823 GCAACGACACCACTACTTCCGCTTACAGACACCCCTGGGGGTATTTGATTTCAACAGAT 2882
QY 3070 TCCACTGCAATTTTCAACAGTGAAGTGGGAGCACTCAATAACAATTGGGGATTC 3129
Db 2883 TCCACTGCAATTTTCAACAGTGAAGTGGGAGCACTCAATAACAATTGGGGATTC 2942
QY 3130 GGGCCAAAGAGACTCAACTTCAAGCTCTTCAACATCCAAAGTCAAGAGGTCAAGAGATG 3189
Db 2943 GGGCCAAAGAGACTCAACTTCAACATCCAAAGTCAAGAGGTCAAGAGATG 3002
QY 3190 ATGGCGTCAAGCAATGCTAATTAATTAACCTTACAGACGAGTTCAAGTCTTGTGGACTCG 3249
Db 3003 ATGGCGTCAACCAATGCTAATTAATTAACCTTACAGACGAGTTCAAGTCTTGTGGACTCG 3062
QY 3250 AGTACCACTTCCCGTACGTCTCGGCTGTGGGACAGAGGTGCTCCCTCCGTTCCCG 3309
Db 3063 AGTACCACTTCCCGTACGTCTCGGCTGTGGGACAGAGGTGCTCCCTCCGTTCCCG 3122
QY 3310 CGGACGTGTCATATTCGAGATGCGGCTAACCTTAACGCTCAACATATGAGCCAGGCA 3369
Db 3123 CGGACGTGTCATATTCGGAATACGCTAACCTTCAAGGCTTCAAGATGAGCCAGGCA 3182
QY 3370 TGGAGCTCATCTTTTACTGCTCGTGAATATTTCCATGCGAGATCTGAGAAAGGCA 3429
Db 3183 TGGAGCTCATCTTTTACTGCTCGTGAATATTTCCCTTCAAGATCTGAGAAAGGCA 3242
QY 3430 ATTACTTACCTTCAAGTCAACCTTCAAGAGAGTGGCTTTCACAGAGAGTCAAGCGGACA 3489
Db 3243 ACAACTTACCTTCAAGTCAACCTTCAAGAGAGTGGCTTTCACAGAGAGTCAAGCGGACA 3302
QY 3490 GCCAGAGCTGAGACGGCTGATGAATCTCTCATGACAGTACGTAATTAACCTGAGACA 3549

Db	3303	GCACAGCCTGGACCGGCTGATGAATCCTCTCATGACCAATACTGTATTTACTGAAACA	3362
Oy	3550	GAACTCACAAATCAGTCCGGAAGTGGCCAAAACAAGACTTGTGTTTAAAGCCGTGGGTCTC	3609
Db	3363	GAACTCAAAATCAGTCCGGAAGTGGCCAAAACAAGACTTGTGTTTAAAGCCGTGGGTCTC	3422
Oy	3610	CAGCTGGATGTCTGTGTAGGCCCAAAAATGCGCTACCTGGACCCCTGTTATCGGCAGACG	3665
Db	3423	CAGCTGGATGTCTGTGTAGGCCCAAAAATGCGCTACCTGGACCCCTGTTATCGGCAGACG	3482
Oy	3670	GCCTTCTAAAACAAAAACAGACAACAACAAGCACTTTACCTGACCTGGTCTTCAA	3729
Db	3483	GCCTTCTAAAACAAAAACAGACAACAACAAGCACTTTACCTGACCTGGTCTTCAA	3542
Oy	3730	AATATTAACCTTAATGGCGGTGATCTTAATTAACAACCTGGACACTGCTATGCGCTCACACA	3789
Db	3543	AATATTAACCTTAATGGCGGTGATCTTAATTAACAACCTGGACACTGCTATGCGCTCACACA	3602
Oy	3790	AAGACGACAAAGACAAAGTTCTTTCCATGAGGGGTGATGATTTTGGAAAAGAGACG	3849
Db	3603	AAGACGACAAAGACAAAGTTCTTTCCATGAGGGGTGATGATTTTGGAAAAGAGACG	3662
Oy	3850	CCGGAGCTTCAACACATGCACTATGACAAATGTCAATGATACAGACGAAAGGAAATCAAAAG	3909
Db	3663	CCGGAGCTTCAACACATGCACTATGACAAATGTCAATGATACAGACGAAAGGAAATTAAG	3722
Oy	3910	CCACTTAACCCCGTGGCCACCGAAGATTTGGACCTGTGGCAGTCAATCTCCAGACAGACA	3965
Db	3723	CCACTTAACCCCGTGGCCACCGAAGATTTGGACCGTGTGGCAGTCAATTTCCAGACAGACA	3782
Oy	3970	GCACAGACCCCTGGCCACCGAGATGTGCATGTTATGGAGCCTTAACCTGGAATGGTGTGC	4029
Db	3783	GCACAGACCCCTGGCCACCGAGATGTGCATGTTATGGAGCATTACTGGCATGGTGTGC	3842
Oy	4030	AAGACAGACGATATCCTGCAGGGTCTTAATTTGGCCAAAATTCCTACAACGATGGAC	4089
Db	3843	AAGATAGAGAGGTGATCCTGCAGGGTCCCAATTTGGCCAAAATTCCTACAACAGATGGAC	3902
Oy	4090	ACTTTCAACCCGCTCTCTCAATGGGGGCTTTGGACTTAAGCAACCGGCTCTCAAGATCC	4149
Db	3903	ACTTTCAACCCGCTCTCTCTTAATGGGGGCTTTGGACTTAAGCAACCGGCTCTCAAGATCC	3962
Oy	4150	TCATCAAAAACACGCGCTGTCTCGTGGAAATCCTCCGCGAGATTTTCGCTCAAAAGTTTG	4209
Db	3963	TCATCAAAAACACGCGCTGTCTCGTGGAAATCCTCCGCGGGAAGTTTCACTCAAAAGTTTG	4022
Oy	4210	CTTCATTATCAACCAATATTCACACGACAATGACGCTGGAGATTGAATGGAGCTGC	4265
Db	4023	CTTCATTATCAACCAATATTCACACGACAATGACGCTGGAGATTGAATGGAGCTGC	4082
Oy	4270	AGAAAGAAAACAGCAAAACGCTGGAAATCCGAAAGTCAGATATACATCTAACATGCAAAAT	4329
Db	4083	AGAAAGAAAACAGCAAAACGCTGGAAATCCGAAAGTCAGATACATCAATTAATGCAAAAT	4142
Oy	4330	CTGCCAACGTTGATTTCACTGTGACAACAATGCACTTTAATAGGCGTCCGCCCAATG	4389
Db	4143	CTGCCAACGTTGATTTACTGTGGACAACAATGCACTTTAATAGGCGTCCGCCCAATG	4202
Oy	4390	GCAACCCGTTACTCACCCCGTCCCTGTATATGTGTAAATCAATAAACCGGTTAATTCG	4449
Db	4203	GCAACCCGTTACTTAACCCGTCCTCCGTATATTAACGTTAATCAAAATAACCGGTTGATTCG	4262
Oy	4450	TGTCAGTTGAACTTTGTGTCATATGCTCACTTAATATCTTAATCTGTGTCACATAGCAACCGGT	4509
Db	4263	TTTCAAGTTGAACTTTGTGTCATATGCTCTCTCTCTTATCTTAATC-GGTTAACATGGTTATAGCT	4321
Oy	4510	TACACATTAACTGTTAAGTGGCTT 4535	
Db	4332	TACACATTAACTGTTGTTGGCTT 4347	

ID	AD676502 standard; DNA; 4721 BP.
AC	AD676502;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Adeno-associated virus (AAV) related DNA, SEQ ID No 1.
XX	
KW	adeno-associated virus; AAV; cytostatic; antiporiatic; antirheumatic;
KW	antiarthritic; neuroprotective; antidiabetic; antithyroid;
KW	dermatological; antiinflammatory; gene therapy; vaccine;
KW	hyperproliferative; cancer; psoriasis; autoimmune disease;
KW	rheumatoid arthritis; multiple sclerosis; diabetes;
KW	autoimmune thyroiditis; scleroderma; Crohn's disease; gene; ds.
XX	
OS	Adeno-associated virus 7.
XX	
PN	EP110571-A2.
XX	
PD	14-MAY-2003.
XX	
PF	12-NOV-2002; 2002EP-00257826.
XX	
PR	13-NOV-2001; 2001US-0350607P.
XX	
PR	17-DEC-2001; 2001US-0341117P.
XX	
PR	01-MAY-2002; 2002US-0377066P.
XX	
PR	05-JUN-2002; 2002US-0386675P.
XX	
PA	(TYPE-) UNIV PENNSYLVANIA.
XX	
PI	Gao G, Wilson JM, Alvira M;
XX	
DR	WPI: 2003-450984/43.
XX	
DR	P-PSDB; AD676503.
XX	
PT	Detecting adeno-associated virus sequences in a sample, useful for e.g.
XX	preventing or treating hyperproliferative or autoimmune diseases,
PT	comprises subjecting a sample having a DNA to amplification via
XX	polymerase chain reaction.
XX	
PS	Claim 17; SEQ ID NO 1; 419pp; English.
XX	
XX	The invention relates to a novel method for detecting adeno-associated
CC	virus (AAV) sequences in a sample, which comprises subjecting a sample
CC	containing a DNA to amplification via a polymerase chain reaction (PCR).
CC	The AAV sequence have the following activities: cytostatic,
CC	antiporiatic, antirheumatic, antiarthritic, neuroprotective,
CC	antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV
CC	sequence can be used in gene therapy or as part of a vaccine to treat
CC	disorders. The method is useful in detecting and/or identifying AAV
CC	sequences and isolating novel sequences that are identified. The
CC	sequences may be used e.g. for preventing or treating hyperproliferative
CC	conditions such as cancers and psoriasis, and other autoimmune diseases
CC	like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
CC	thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence
CC	represents an AAV related DNA sequence of the invention.
XX	
SQ	Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
XX	
Query Match	78.5%; Score 3678.4; DB 10; Length 4721;
Best Local Similarity	87.5%; Pred. No. 0; Mismatches 541; Indels 52; Gaps 8
Matches 4135; Conservative	0; Mismatches 541; Indels 52; Gaps 8
Db	
1	TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGCGGCGACCAAGGTGCGC 60
1	TTGGCCACTCCCTCTATGCGCGCTGCTGCTCGGTGGGCGCTGGGACCAAGGTGCGC 60
Qy	CGAGCCCGGGGTTTGGCCCGCGCGCTTCAGTACCGAGCGAGCGCGGAGAGGAGTG 120
61	AGACGGCGAGAGCTGCTGCTGCGCGCGCCACCGAGCGAGCGAGCGCGCATTAAGGAGTG 120
121	GCACAATCATCATCAGAGGGGTTCTCTGAGG-----GGTGAAGTGTGAC 164

Dh 121 GCCAACTCCATCACTAGGGGTACCGGAAGGCGCTCCACGCTGCGGCTGACGCGCTAC 180
Qy 165 GTGAATTACGTCATAGGGTTAGGGAGGCTCTGTATTAGAGTCACTGAATG-TTTTCCG 223
Db 181 GTAATACGTCATAGGG---GAGTGTCTGTATTAGCTGTACAGTAAAGCTTTTCCG 237
Qy 224 ACATTTTGCAGACACATGTGTGTCAGCTGTGGTATTAAAGCCGAGTGAACAAGGAGTC 283
Db 238 ACATTTTGCAGACACATGTGTGTCAGCTGTGGTATTAAAGCCGAGTGAACAAGGAGTC 297
Qy 284 TCCATTTTGAACCGGAGGTTTGAACGCGACAGCCGATGCGGGTTTAAAGATTG 343
Db 298 TCCATTTTGAACCGGAGGTTTGAACGAGACAGACGATGCGGGTTTAAAGATTG 357
Qy 344 ATTAAGTCCCGACGACCTTGAAGAGATCTGCCGCAATTTCTGACAGCTTTGTGAAC 403
Db 358 ATCAAGGTCGAGAGCACTGAGACAGCACTGCGGCAATTTCTGACTCGTTGTGAAC 417
Qy 404 TGGGTGGCCGAGAAAGAAATGGAGTGTGCGGCAATTTGACATGAGCTGAATCTGATT 463
Db 418 TGGGTGGCCGAGAAAGAAATGGAGTGTGCGGCAATTTGACATGAGCTGAATCTGATT 477
Qy 464 GAGCAGGACCCCTGACCGTGTGCGAGAAAGCTGACGCGCATTTCTGTCTCACTGCGC 523
Db 478 GAGCAGGACCCCTGACCGTGTGCGAGAAAGCTGACGCGCATTTCTGTCTCAATGCGC 537
Qy 524 CGCTGAGTAAGGCCCCGAGAGCCCTCTTTCTTTGTTCACTTGAAGAGGCGAGTCTAC 583
Db 538 CGCTGAGTAAGGCCCCGAGAGCCCTCTTTCTTTGTTCACTTGAAGAGGCGAGTCTAC 597
Qy 584 TTCCACCTCCATTTCTGTGTGAGACCAAGGAGGCAATCCATGTGTCTGGGCGCTTC 643
Db 598 TTCCACCTCCATTTCTGTGTGAGACCAAGGAGGCAATCCATGTGTCTGGGCGCTTC 657
Qy 644 CTGAGTCAGATTAGCGACCAAGCTGTGTGAGACCACTCACTGCGGGATGACCGACCTG 703
Db 658 CTGAGTCAGATTAGCGAGAACTGTGTCAAGCACTCACTGCGGGATGACCGACCTG 717
Qy 704 CCCAATGTGTGCGGTGACCAAGACGCTGATATGCGCGGAGGGGGAAACAAGTGTG 763
Db 718 CCCAATGTGTGCGGTGACCAAGACGCTGATATGCGCGGAGGGGGAAACAAGTGTG 777
Qy 764 GAGAGTGTATCATCCCCCACTACTCTGCGCAAGACTGAGGCTGCAATGAGGCG 823
Db 778 GAGAGTGTATCATCCCCCACTACTCTGCGCAAGACTGAGGCTGCAATGAGGCG 837
Qy 824 TGAATCAATGAGAGTATATAAGCGCTGTAACTGTGCGGACGCGCAACGCGTC 883
Db 838 TGAATCAATGAGAGTATATAAGCGCTGTAACTGTGCGGACGCGCAACGCGTC 897
Qy 884 GTGGCGCAGACTGACCTGACCTGACGCGCAAGCCAGAGAGCAACAAGAGATCTGAAC 943
Db 898 GTGGCGCAGACTGACCTGACCTGACGCGCAAGCCAGAGAGCAACAAGAGATCTGAAC 957
Qy 944 CCCAATGTGTGCGGCTGTATCCGCTCAAAACCTCCGACGCTCATGTGAAGCTGTG 1003
Db 958 CCCAATGTGTGCGGCTGTATCCGCTCAAAACCTCCGCTCAATGTGAAGCTGTG 1017
Qy 1004 GGGTGTGTGTGACCGGGGATCACTCGAGAGAGAGTGAATCCAGAGACAGAGCC 1063
Db 1018 GGGTGTGTGTGACCGGGGATCACTCGAGAGAGAGTGAATCCAGAGACAGAGCC 1077
Qy 1064 TCGTATCTTCTTCAAGCGCGCTTCAACTGCGGTGCCAGATCAAGGCGCTGTGAC 1123
Db 1078 TCGTATCTTCTTCAAGCGCGCTTCAACTGCGGTGCCAGATCAAGGCGCTGTGAC 1137
Qy 1124 AATGCGGCAAGATCATGTGCGCTGACCAAAATCGGCGCGCACTGATGAGCGCGCT 1183
Db 1138 AATGCGGCAAGATCATGTGCGCTGACCAAAATCGGCGCGCACTGATGAGCGCGCT 1197
Qy 1184 CCGCGCGCAATTAACCAACCGCATTTTACCGCATCTGAGAGTGAACGCGTACGAC 1243
Db 1198 CCGCGCGCAATTAACCAACCGCATTTTACCGCATCTGAGAGTGAACGCGTACGAT 1257

Qy 1244 CTTGCTTACGCGGCTCCGTCTTTCTGCGCTGGGCCCCAGAAAGATTGGAACCGAAC 1303
Db 1258 CTTGCTTACGCGGCTCCGTCTTTCTGCGCTGGGCCCCAGAAAGATTGGAACCGAAC 1317
Qy 1304 ACCATCTGAGTGTGTGGGCGGGACCAACGAGGCAAGACCAATGTGAGAGCCATGCGC 1363
Db 1318 ACCATCTGAGTGTGTGGGCGGGACCAACGAGGCAAGACCAATGTGAGAGCCATGCGC 1377
Qy 1364 CAGCGCTGCTTTCTACGCGTGTGCTGACCAATGAGAACTTTCCCTTCAAGAT 1423
Db 1378 CAGCGCTGCTTTCTACGCGTGTGCTGACCAATGAGAACTTTCCCTTCAAGAT 1437
Qy 1424 TGCCTGCAAGATGTGTATCTGTGGAGAGAGGCAAGATGACGCGCCAGTGTGAG 1483
Db 1438 TGCCTGCAAGATGTGTATCTGTGGAGAGAGGCAAGATGACGCGCCAGTGTGAG 1497
Qy 1484 TCGGCAAGGCAATTCCTGCGGCGAGCAAGGTGTGCGCTGAGCAAAAGTGCAGTCTC 1543
Db 1498 TCGGCAAGGCAATTCCTGCGGCGAGCAAGGTGTGCGCTGAGCAAAAGTGCAGTCTC 1557
Qy 1544 GCCAGATCGATCCACCCCGTGTATGTCACTTCAACACCAATGTGCGCGTGAAT 1603
Db 1558 GCCAGATCGATCCACCCCGTGTATGTCACTTCAACACCAATGTGCGCGTGAAT 1617
Qy 1604 GACGGAAACAGACACACCTTGTAGACCAAGACCGCTTGCAGAGCCGGAATTTCAATTT 1663
Db 1618 GACGGAAACAGACACACCTTGTAGACCAAGACCGCTTGTGAGAGCCGGAATTTCAATTT 1677
Qy 1664 GAATCAACCCGCGCTGTGAGCATGATTTTGGCAAGGTGAACAAGCAGAAATGCAAGAG 1723
Db 1678 GAATCAACCCGCGCTGTGAGCATGATTTTGGCAAGGTGAACAAGGTGCAAGAG 1737
Qy 1724 TTCTTCGCTGTGGGCGAGATCAAGTACCGAGTGTGCGATGATTTCTACGTCAAGAAG 1783
Db 1738 TTCTTCGCTGTGGGCGAGATCAAGTACCGAGTGTGCGATGATTTCTACGTCAAGAAG 1797
Qy 1784 GGTGAGACCAACAACAACCGGCCCCGATGACGCGGATTAAGAGGACCCAGCGGCC 1843
Db 1798 GGTGAGACCAACAACAACCGGCCCCGATGACGCGGATTAAGAGGACCCAGCGGCC 1857
Qy 1844 TGCCCTCAGTGTGCGGATTCATGAGTCAAGCGCGGAGAGCTCGGTGTGACTTTGCC 1903
Db 1858 TGCCCTCAGTGTGCGGATTCATGAGTCAAGCGCGGAGAGCTCGGTGTGACTTTGCC 1917
Qy 1904 GACAGTACCAAAACAATGTCTGTGACGCGGCGATGTCTTCAAGTGTCTTCCCTGC 1963
Db 1918 GACAGTACCAAAACAATGTCTGTGACGCGGCGATGTCTTCAAGTGTCTTCCCTGC 1977
Qy 1964 AAAACATGCGAGAGATGAATCAAGATTTCAACTTTGCTTCAAGCAGGACCAAGAGAC 2023
Db 1978 AAAACATGCGAGAGATGAATCAAGATTTCAACTTTGCTTCAAGCAGGAGTCAAGAGAC 2037
Qy 2024 TGTTCAGAAATTTTCCCGGCGGTGTGAGATTTCAACCGGTCGCAAAAGAGAGCGAT 2083
Db 2038 TGTTCAGAAATTTTCCCGGCGGTGTGAGATTTCAACCGGTCGCAAAAGAGAGCGAT 2097
Qy 2084 CGGAACTGTGTGCAATTCATCTGCTGTGGGCGGCTCCGAGATGTGTGCTGCGCC 2143
Db 2098 CGGAACTGTGTGCAATTCATCTGCTGTGGGCGGCTCCGAGATGTGTGCTGCGCC 2157
Qy 2144 TGGATCTGTGCAAGTGTGATCTGATGATCTGTGTTCTGAGCAATTAATGACTTAAAC 2203
Db 2158 TGGATCTGTGCAAGTGTGATCTGATGATCTGTGTTCTGAGCAATTAATGACTTAAAC 2217
Qy 2204 AGGATGCTGTGCGAGATTTATCTTCCAGATTTGGCTGAGAGCAACTCTCTGAAGGAT 2263
Db 2218 AGGATGCTGTGCGAGATTTATCTTCCAGATTTGGCTGAGAGCAACTCTCTGAAGGAT 2277
Qy 2264 TCGCAGTGTGTGAGACTTGAACCTGAGGCCCCGAAACCCAAAGCCAAACGAGCAAAAGCA 2323
Db 2278 TCGCAGTGTGTGAGACTTGAACCTGAGGCCCCGAAACCCAAAGCCAAACGAGCAAAAGCA 2337

OY	2324	GGAGCAGCGCCGGGGTCTGGGTGCTTCCGTGCTACAGAGTACCTCGGACCCCTTCAACGGACT	2383
Db	2338	GGACAAACGGCCGGGGTCTGGGTCTTCTGGCTCAAGATACCTCGGACCTTCTCAACGGACT	2397
OY	2384	CGACAGAGGGGAGCCCTCAACGCGCGCGAGATGACAGCGGCGCTCGAGCAGCAAGGCGCTA	2443
Db	2398	CGACAGAGGGGAGCCCTCAACGCGCGCGAGATGACAGCGGCGCTCGAGCAGCAAGGCGCTA	2457
OY	2444	CGACAGCAGCTCAAAAGCGGCTGACATCCGTACCTGCGGTATATACACGCGCGACGCCGA	2503
Db	2458	CGACAGCAGCTCAAAAGCGGCTGACATCCGTACCTGCGGTATATACACGCGCGACGCCGA	2517
OY	2504	GTTTCAGAGGGCTCGCAAGAAAGTACGTCTTTTGGGGGGCAACCTCGGGCGAGCAGTCTT	2563
Db	2518	GTTTCAGAGGGCTCGCAAGAAAGTACGTCAATTTGGGGGGCAACCTCGGGCGAGCAGTCTT	2577
OY	2564	CCAGGCGCAAGAAAGAGGTTCTCGAACCCTTTTGCTGGTTGAGAGAGGTGTATAGACGGC	2623
Db	2578	CCAGGCGCAAGAAAGGGGTTCTCGAACCCTCGGTCTGGTTGAGAGAGGCGTTAAGACGGC	2637
OY	2624	TCTCGGAAAAGAAACGTCCGGTAGAGCAGTGCACACA--AGAGCCAGACTCTCTCTCGGG	2680
Db	2638	TCTCGGAAAAGAAAGACCGGTAGAGCGCTCACCTAGCGTTCCCGCGACTCTCTCAACGGG	2697
OY	2661	CATTGGCAGACAGGGCCGACGCCCTCGTAAAAAGATCAATTTTGGTCAATTCGCGA	2740
Db	2698	CATTGGCAGAAAGGCGCAGACGCCCGCAGAAAGAGCTCAATTTGGTCAATTCGCGA	2757
OY	2741	CTCAGAGTCAGTCCCGCAGCCCAACCTCTCGAGAAACCTCAGCAACCCCGCTGCTGT	2800
Db	2758	CTCAGAGTCAGTCCCGCAGCCCTCAACCTCTCGAGAAACCTCAGCAGGCGCCTTAAGT	2817
OY	2801	GGGACCTTACATAATGCTTACAGCGGTGCGCACAAATGCGAGCAATTAACGAAGCGC	2860
Db	2818	GGGATCTGTGTAAGTGGCTGCAGGCGGTGGCGCACAAATGCGAGCAATTAACGAAGGTG	2877
OY	2861	CGACGAGATGGGTATATGCTCCTAGGAAATTTGGCATTTGCGATTCCACATGCTGGCGACAG	2920
Db	2878	CGACGGAATGGGTATATGCTCCTAGGAAATTTGGCATTTGCCATTGCCATGCTGGCGACAG	2937
OY	2921	AGTCATCACCAACAGCACCCCGAACATGGGCGCTTGGCCACTATTAACAACAACCTCTCA	2980
Db	2938	AGTCATTAACAACAGCACCCCGAACCTGGGCGCTTGGCCACTTAACAACAACCTCTTAACA	2997
OY	2981	GCAATATCTCCAGTGTCTTCAACGGGGGCGAGCAACGACCAACCTATCTCGGCTACAGAC	3040
Db	2998	GCAATATCTCCAGTGAAACTGCAAGGTATACCAAGCAACAACCTATCTCGGCTACAGAC	3057
OY	3041	CCCCCGGGGGTATTTTGAATTTCAACAGATTTCACTGCCATTTCTCACACGTGACTGGCA	3100
Db	3058	CCCCCGGGGGTATTTTGAATTTCAACAGATTTCCACTGCCATTTCTCACACGTGACTGGCA	3117
OY	3101	GCGACTCATCAACAACAATTTGGGGGTTCCGGGCCAAGAGCTCAACCTCAAGCTCTTCA	3160
Db	3118	GCGACTCATCAACAACAATTTGGGGGTTCCGGGCCAAGAGCTCGGGTTCAAGCTCTTCA	3177
OY	3161	CATCCAAATCAAGAGAGTCAACGACGAATGATGCGCTCAACGACATCGCTAATTAACCTTAC	3220
Db	3178	CATCCAAATCAAGAGAGTCAACGACGAATGATGCGGTTACGACATCGCTAATTAACCTTAC	3237
OY	3221	CAGCAGCGTTCAAGCTTGTGGAGCTGGGAATCAAGTTCCCGTACGTCTCGGCTCTGC	3280
Db	3238	CAGCAGCGATTCAGGTATCTCGGACTCGGAATACCAAGCTGCGCGTACGTCTCGGCTCTGC	3297
OY	3281	GCACCAAGGAGTCCCTCCCTCCGTTCCGGCGGAGCGTCTTCAATGATTCGCGAGTACGGCTA	3340
Db	3298	GCACCAAGGAGTCCCTCCCTCCGTTCCGGCGGAGCGTCTTCAATGATTCGCGAGTACGGCTA	3357
OY	3341	CCTAACGCTCAACAATGCGACGACGAGGAGTGGGAGCGCTATCTTTTACTCGCTGAGATA	3400
Db	3358	CCTGACTCTCAACAATGCGACGAGTCACTGTGTGGAGGTTCTCTCTTCACTGCTGGAGTA	3417
OY	3401	TTTCCCATCGAGATGCTTGAGAACGGGCAATTACTTTACCTTCAAGCTACACCTTCGAGGA	3460

D	b	3418	CTTCCCTCTCAGATGCTGAGAAAGGGCAACACTTTGAAGTTCAAGCTACAGCTTCGAGAA	3477
O	y	3461	CGTGCCTTTCCACAGCAGCTACGGCACAAGCCAGAGCCTGAGCCGGCTGAATGAATCTCT	3520
D	b	3478	CGTCCCTTTCCACAGCAGCTACGCAACAGCCAGAGCCTGAGCCGGCTGAATGAATCCCT	3537
O	y	3521	CATGACACAGTACTCTGTATTACCTGAACAGAACTCAAACTCAATCACTCCGGA---AGTGGCCA	3577
D	b	3538	CATGACACAGTACTCTGTACTACTGGCCAGAAACAAGATTAACCCAGAGGGCAAGCTGG	3597
O	y	3578	AAACAAGAACTGTGCTGTTTACCCTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAA	3637
D	b	3598	CAATCGGGAACGTAGTTTATCCAGGGCGGGCTTCAACTATGGCCGAACAAGCCAAAGA	3657
O	y	3638	CTGGCTACCTGGAACCTGTATTACGGGAGCAGCGCGTTTCTAAAACAAAACAAGACA	3697
D	b	3658	TTGTGTAACGTGACCTTGCTTCGGGCAACAAAGATCTCCAAAACCGTGATCAAAAACA	3717
O	y	3698	CAACAGCAACTTTTACCTGACCTGTGCTCTAAAATATTAACCTTAATAGGGGTGAATCTAT	3757
D	b	3718	CAACAGCAACTTTTGTCTTGGACTGGTGGCACCAATTAACCTGAACGGCAGAAATCTGTT	3777
O	y	3758	AATCAACCCCTGGGCACTGCTATGGCTGCACAACAAAGACGAACAAAGACAAGTTTCCAT	3817
D	b	3778	GGTTAATCCGGCGCTCGCCATGGCACTCACAGAGACAGAGAGACGGCTTTTCCATC	3837
O	y	3818	GAGCGGTGTCAATGTTTTTGGAAAAGAGACCGCCGAGCTTCAACACTGCATTGACAA	3877
D	b	3838	CAGCGGAGTCCGTATTTTTGGAA---AAACTGGAGCAACTAACAACTCACTATGGAAAA	3894
O	y	3878	TGTATGATGATCACAGACGAAGAGAAATCAAAAGCATTAACCCCGTGGCCACCGAAGATT	3937
D	b	3898	TGTGTTAATGACAAATATAAGAAATTCGTCTTACTAACTCGTATGCCACGGAAGATA	3954
O	y	3938	TGGGACTGTGGCAGTCAATCTCCAGACACAGACAGACACCCCTGGCACCGAGATGACA	3997
D	b	3958	CGGATATGTCAGACGCAACTTACAGCGGCTAATATCTGCAGCCACAGACAAAGTTGTCAA	4014
O	y	3998	TGTTATGGGAGCCCTTACCTGGAATGTGTGGCAAGACAGAGCGTATACCTGACGGGTCC	4057
D	b	4018	CAACACAGGAGCCTTACTGTGGCAGTGTCTGGCAAGAACGGGACGTGTACTGTGACGGTTC	4074
O	y	4058	TATTTGGGCCAAATTCCTCAACAGGATGACACTTCAACCCGCTCTCTCATGGGCGG	4117
D	b	4078	CATCTGGGCCAAGATTCCTCAACGAGATGGCACTTCAACCCGCTCTCTTGTGATGGGCGG	4134
O	y	4118	CTTTGACTTAAGACCCGCTCTCTCGATTCCTATCAAAAACAACGCTGTCTCTGGAA	4177
D	b	4138	CTTTGACTTAACATCCGCTCTCTCGATTCCTATCAAAAACAACGCTGTCTCTGGAA	4194
O	y	4178	TCTCTCCGAGAGTTTTCGCTACAAAGTTTGCTTCAATCATCAACCAAGTATTCACAGG	4237
D	b	4198	TCTCTCCGAGAGTTTACTCTCTCGCAAGTTTGCTGTTCATCAACAGTACAGACACCGG	4254
O	y	4238	ACAAAGTACGCTGAGATTGAATGGAGCTGCAGAAAGAAAACAGCAACGCTGGAAATCC	4297
D	b	4258	ACAAGTACGCTGAGAAATCGAGTGGAGCTGCAGAAAGAAAACAGCAACGCTGGAAATCC	4314
O	y	4298	CGAAGTCAGAGTATCACTAATCTATGGAATATCGCAAGTGTGATTTCACTGAGCA	4357
D	b	4318	GGAAATTCAGTACCTTCACACTTTGAAAGACAGATGCTGTGGAATTTGCCGTTGACAG	4374
O	y	4358	CAATGCACTTTATCTAGAGCTCGCCCAATTTGGCACCCGTATCTCAACCGCTCCCTGTA	4417
D	b	4378	CCAGGAGTGTACTCTAGAGCTCGCCCAATTTGGCACTCGTATCTCAACCCGTAATCTGTA	4434
O	y	4418	ATTGTGTGTAAATCAATAAACCGGTATATTGTGTACAGTTGAACCTTGTGTCTATGTCT	4477
D	b	4438	ATTGCATGTATATCAATAAACCGGTGATTCGTTTCAAGTTGAACCTTGTGTCTCTGTGCT	4494
O	y	4478	TATTAATCTATCTGTGTAACCAATAGCAACCGGTATCAATTAATCTGTAGTGTGGCTTGG	4537

Dh 898 GTGCGCAGCACTTGACCCACGTCAGCCAGCAGAGAGCAAAACAAAGAAATCTGAAAC 957
Qy 944 CCGAATTTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGACGCTCATATGAGCTGTC 1003
Db 958 CCGAATTTCTGACGCGCCTGTCATGAGTCAGAAACCTCCGCGCTCATATGAGCTGTC 1017
Qy 1004 GGGTGGCTGTGGA CCGGGGATCACTCCGAGAAAGAGTGGATCCAGAGGACCAAGCC 1063
Db 1018 GGGTGGCTGTGGA CCGGGGATCACTCCGAGAAAGAGTGGATCCAGAGGACCAAGCC 1077
Qy 1064 TCGTACATCTCTTCAACGCCGCTTCAACTCGGGTCTCCGATTCAGAGCCGCTGTGAC 1123
Db 1078 TCGTACATCTCTTCAACGCCGCTTCAACTCGGGTCTCCGATTCAGAGCCGCTGTGAC 1137
Qy 1124 AATGCGGCAAGATCATGGGCGCTGACCAATCCGGGCCGACTACTGTGTAGGCCGCT 1183
Db 1138 AATGCGGCAAGATCATGGGCGCTGACCAATCCGGGCCGACTACTGTGTAGGCCGCT 1197
Qy 1184 CCGCCCGCGACATTTAAACCAACCGCATTTTACGCACTCTGAGCTGAA CCGCTACGAC 1243
Db 1198 CTGCCCCGGGACATTTAAACCAACCGCATTTTACGCACTCTGAGCTGAA CCGGTACGAT 1257
Qy 1244 CTGTCTTACCGCGCTCGTCTTTCTCGGCTGGGCCAGAAAGGTTGGAAAACGCAAC 1303
Db 1258 CTGTCTTACCGCGCTCGTCTTTCTCGGCTGGGCCAGAAAGGTTGGAAAACGCAAC 1317
Qy 1304 ACCATCTGGCTGTTTGGGCGGGCCACCA CCGGCAAGAACCAATCGGGGAAGCCATGCGC 1363
Db 1318 ACCATCTGGCTGTTTGGGCGGGCCACCA CCGGCAAGAACCAATTTGGGAAGCATGCGC 1377
Qy 1364 CAGCGCGTGCCTTTCTAGGCTGCGTCACTGAA CCAATGAAACTTTCCCTTCAACGAT 1423
Db 1378 CAGCGCGTGCCTTTCTAGGCTGCGTCACTGAA CCAATGAAACTTTCCCTTCAACGAT 1437
Qy 1424 TCGCTCGCAAGATGTGTATCTGTGTGGAGAGAGGCAAGATGACGGCCCAAGTGTGTGAG 1483
Db 1438 TGCCTCGCAAGATGTGTATCTGTGTGGAGAGAGGCAAGATGACGGCCCAAGTGTGTGAG 1497
Qy 1484 TCGCCCAAGGCACTTCTCGGCGGAGCAAGGTGCGCGTGAACAAAAGTGCAGTCTGCC 1543
Db 1498 TCGCCCAAGGCACTTCTCGGCGGAGCAAGGTGCGCGTGAACAAAAGTGCAGTCTGCC 1557
Qy 1544 GCCCAGATCGATCC CACCCCGGTGATGCTCACTTCAAC CACCAACATGTGCGCGTGAAT 1603
Db 1558 GCCCAGATCGACCC CACCCCGGTGATGCTCACTTCAAC CACCAACATGTGCGCGTGAAT 1617
Qy 1604 GACGGGAACAGCA CCACTTGAAGCA CCAAGACCGTGTGAGAC CCGATTTTCAATTT 1663
Db 1618 GACGGGAACAGCA CCACTTGAAGCA CCAAGACCGTGTGAGAC CCGATTTTCAATTT 1677
Qy 1664 GAATCTCA CCGCGCTGTGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAG 1723
Db 1678 GAATCTCA CCGCGCTGTGTGAGCA CCACTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAG 1737
Qy 1724 TTCTTTCGCTGGGCGCAGGATCACGTGA CCGAGGTGGCGCATGATTCTACGTCAAAAG 1783
Db 1738 TTCTTTCGCTGGGCGCAGGATCACGTGA CCGAGGTGGCGCATGATTCTACGTCAAAAG 1797
Qy 1784 GGTGAGACCAAC CAGACCCGCCCGCATGACCGCGATTAAGAGCAGGCCAAGCGGCC 1843
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Qy 1844 TGCCCTCAGTGTGGGATTCATGACGTCAGACGGAGGAGGCTCCGGTGGACTTTGGC 1903
Db 1858 TGCCCTCAGTGTGGGATTCATGACGTCAGACGGAGGAGGCTCCGGTGGACTTTGGC 1917
Qy 1904 GACAGGTACCAAAA CAAATGTTCTGTCA CCGGGGCAATGCTTCAATGCTGTTCCCTGC 1963
Db 1918 GACAGGTACCAAAA CAAATGTTCTGTCA CCGGGGCAATGCTTCAATGCTGTTCCCTGC 1977
Qy 1964 AAAACATGGGAGAAATGAAATCAAAATTTGCAATTTGCTTCAAGCACGGGACCAAGAGAC 2023
Db 1978 AAAACGTGGAGAAATGAAATCAAAATTTGCAATTTGCTTCAAGCACGGGGGTCAAGAGAC 2037

Qy 2024 TGTTCAGAAATGTTTCCCGCGCTGTCAAGATCTCAACCGGTCTGTCAAGAAAGAGACGTAT 2083
Db 2038 TGTTCAGAAATGTTTCCCGCGCTGTGTCAAGATCTCAACCGGTCTGTCAAGAAAGAGACGTAT 2097
Qy 2084 CCGAAACTGTGTCCATTCATCTGTGTGGGCGGGCTCCGAGATTTGCTTCTGTGGCC 2143
Db 2098 CCGAAACTGTGTCCATTCATCTGTGTGGGCGGGCGCCGACGATTTGCTTCTGTGGCC 2157
Qy 2144 TGGCATCTGTTCACCGTGGATCTGSAATGATGTGTTTCTGAGCAATTAATGACTTAACC 2203
Db 2158 TGGCATCTGTTCACCGTGGATCTGSAATGATGTGTTTCTGAGCAATTAATGACTTAACC 2217
Qy 2204 AGGTATGGCTCCGATGTTATCTTCAGATTGGCTCGAGAGAACCTCTGTGAGGACAT 2263
Db 2218 AGGTATGGCTCCGATGTTATCTTCAGATTGGCTCGAGAGAACCTCTGTGAGGACAT 2277
Qy 2264 TCGGCACTGTGTGACTTGAACCTTGAGGCCCGGAAACCCAAAGCCAA CCGAGAAAAGCA 2323
Db 2278 TCGGCACTGTGTGACTTGAACCTTGAGGCCCGGAAACCCAAAGCCAA CCGAGAAAAGCA 2337
Qy 2324 GGAAGACGGCGGGGTCTGTGCTTCTGTGCTACAGTACCTGGGACCTTCAACGGGACT 2383
Db 2338 GGAAGACGGCGGGGTCTGTGCTTCTGTGCTACAGTACCTGGGACCTTCAACGGGACT 2397
Qy 2384 GGAAGAGGGGAGCCCGTCAACCGCGGATGACGGGCCCTCGAGCAGCAAGGCTTA 2443
Db 2398 GGAAGAGGGGAGCCCGTCAACCGCGGAGAGCGAGGGGCCCTCGAGCAGCAAGGCTTA 2457
Qy 2444 GGAACAGACCTCAAGCGGGGTGACATCTCGTATCTGTGGATTAACCA CCGCGACCGCA 2503
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Qy 2504 GTTTCAGGAGCTGTGCAAGATAGTCTTTTGGGGGCAACCTCGGGGAGAGACTT 2563
Db 2518 GTTTCAGGAGCTGTGCAAGATAGTCTTTTGGGGGCAACCTCGGGGAGAGACTT 2577
Qy 2564 CCAAGCCAAAGAGGGTTCTGAACTTTTGTGTGTGTGAGAAAGTGTCTAAGAGGC 2623
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Qy 2681 CATTTGCAAGACAGGCGCAGCAGCCGCTAAAGAGACCTCAATTTTGTGTGACTGGCGA 2740
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Qy 2921 AGTCATCACACAGCACCCGAAACATGGGCTTGGCCACCTATTAACCA CCACTCTTACAA 2980
Db 2938 AGTCATTAACACAGCACCCGAAACCTGGGCTTGGCCACCTTACAA CCACTCTTACAA 2997
Qy 2981 GCAAAATCTCAGTGTCTTCAACGGGGCGCAGCAAGACCACTACTTCTGGCTACAGAC 3040
Db 2998 GCAAAATCTCAGTGTCTTCAACGGGGCGCAGCAAGACCACTACTTCTGGCTACAGAC 3057
Qy 3041 CCCCTGGGGGTATTTGATTTCAACAGATTCACTGCACTTTTCTCA CAGCTGAGCA 3100
Db 3058 CCCCTGGGGGTATTTGATTTTGAATTTTGAACAGATTCACTGCACTTTTCTCA CAGCTGAGCA 3117

OY	3101	GGAGTACTCAACAACAAATTGGGGATTCGCGCCAAAGACCTCAACTTCAAGCTCTTCA	316
Db	3118	GGAGTACTCAACAACAATTGGGGATTCGCGCCAAAGACCTCAACTTCAAGCTCTTCA	3177
OY	3161	CATCCAAATCAAGAGGTCAACAACAATGATGGCGTCAAGCATCTGCTAAATACCTTAC	322
Db	3178	CATCCAAATCAAGAGGTCAACAACAATGATGGCGTCAAGCATCTGCTAAATACCTTAC	323
OY	3221	CAGCAGGTTCAAGTCTTGTGGAGTCCGAGTACCAAGTTCGGTACGTCCTCGGCTTGC	3280
Db	3238	CAGCAGATTCAGGATTTCTGGGACTCGGAATACCAAGCTCGGTACGTCCTCGGCTTGC	329
OY	3281	GCACTCAGGCTTCCCTCCTCGGCTTCCCGCGGACGTGTTCAATGATTCGCGAGTACGGCTA	334
Db	3298	GCACTCAGGCTTCCCTCCTCGGCTTCCCGCGGACGTGTTCAATGATTCGCGAGTACGGCTA	3357
OY	3341	CCTTAACGCTCAACAAATGGAGCAGGAGCTGGAGGCTCATCCTTTTCTGCGCTGGAAAT	3400
Db	3358	CCTGACTTCAACAAATGGAGTCAAGTCTGTGGAGGCTTCTCTTCTACTGCTGGAGTA	3417
OY	3401	TTTCCCATCGCAGATGCTGAGAACGGGCAATTAATTCTTACCTTCAAGCTACACCTTGAAGA	3466
Db	3418	CTTCCCTCTCAGATGCTGAGAACGGGCAACAATTGATTTACACTTACAGCTTGAAGA	3477
OY	3461	CGTGCCTTTCCAAGAGCTACCGCCACAACCCAGCCTGGAACCGGCTGATGAATCCTT	3520
Db	3478	CGTGCCTTTCCAAGAGCTACCGCCACAACCCAGCCTGGAACCGGCTGATGAATCCTCT	3537
OY	3521	CATGACCAAGTACCTGTTATTAACCTGAACAGAACTACATACATGCTCGGA---AGTGCCCA	3577
Db	3538	CATGACCAAGTACCTGTTATTAACCTGGAACAGAGTAACTCAGAGGCAACGCTGG	3597
OY	3578	AAACAGGACTCTGCTGTTTAAAGCCGTCTTCAGCTGGCAATGCTGTTACAGCCCAAAA	3637
Db	3598	CAATCGGGAACTGCACTTTTACAGAGGGGGGCTTCAACTATATGGCCGAACAAGCAAGA	365
OY	3638	CTGGCTACCTGGAACCTGTTTACCGGACGACGCGCTTTCTAATAACAAAACAGACACA	3697
Db	3658	TTGGTTACTGGAACCTTCTTCGGCAACAAAGATCTTCAAAAACGCTGGAATCAAAA	3717
OY	3698	CAACGCAACTTTACCTGGAACGTGGCTTCAAAATATACTTATATGGGCGTGAATCTAT	375
Db	3718	CAACGCAACTTTGTTGAGACTGGGCAACAAATATACCTGAAACGCAAGAACTCGTT	3777
OY	3758	AATCAACCTTGGAACCTGATATGGCTCTCAACAAGACGCAAGAACAGTCTTTCCTCAT	3817
Db	3778	GGTTAATCCCGGCGTCCGCAATGCACTCAACAGACGACGAGACCGCTTTTCCCATC	3837
OY	3818	GAGCGGTCTCATGATTTTGGAAAGAGAGCGCGGAGCTTCAACACTGCAATTGACAA	3877
Db	3838	CAGCGGAGTCTGATTTTGGAAA---AAATGGAACACTAACAAAACTACATTGGAAAA	3894
OY	3878	TGTCAATGATCAACAGCAAGAGAAATCAAAACCTAACCCCGTGGCCACCGAAAGATT	3937
Db	3895	TGTGTTAATGCAAAATGAAGAAATTCGTCTTACTAATCTGTATGACAGGAAGAAATTA	3954
OY	3938	TGGGACTGTGCAAGTCAATCTCCAGAGCAGCAGCAAGACCTGCGACCGGAGATGTGCA	3997
Db	3955	CGGATATGACAGCAGCACTTACAAAGGCGTAAATCTGACGCCAGACACAAGTTGTCAA	4014
OY	3998	TGTTATGGGACCTTTACCTGGAATGTTGTGCAAGACAGACAGTATACCTGCAAGGCTC	4057
Db	4015	CAACCAAGGAACTTTACTCTGGCATGTCTGGCAGAAACGGGACGTTACTGCAAGGCTC	4074
OY	4058	TATTTGGGCAAAATTCCTCAACAGGAATGACATTTTAAACCCGCTCTCTCAATGGGGGG	4117
Db	4075	CATCGGCAAGATTTCTCAACAGGAATGACATTTTAAACCCGCTCTCTTGAATGGGGGG	4134
OY	4118	CTTTGAACTTAAGCAACCGCTCTCTCAATCTCTCAAAAAACAGCTGTTTCTGCGAA	4177
Db	4135	CTTTGAACTTAACAATCCGCTCTCTCAATCTCTGATCAAGAACTCTCCGTTTCCCGCTAA	4194
OY	4178	TCTTCGCGCAGATTTTGGGCTCAAAAGTTTGCTTCAATTCACCCAGTATTCACAGG	4237

Db	4195	TCCTCGAGAGTGTACTCTCCGCAAGTTGGCTTGTCATCAACAGTACAGCACCGG	4254
Qy	4238	ACAAGTAGCGGTGAGATTGAATGGAGCTGCAGAAAAGAAAACAGCAACGCTGGAAATCC	4297
Db	4255	ACAACTACGCTGGAAATCGAGTGGGAGCTGCAGAAAGAAAACAGCAACGCTGGAAATCC	4314
Qy	4288	CGAAGTCAGATATACATCTTAACTATGCAAAAATCTGCCAAGTTGATTCATCTGGACA	4357
Db	4315	GGAGATTCAGATACACTCCAACTTTGAAAAGCAGACTGGTGTGACCTTTGCCGTTGACAG	4374
Qy	4358	CAATGGAATTTATACCTGAGCCTCGCCCATTTGGACACCGGTAACTCACCCGTCCTGTA	4411
Db	4375	CCAGGTTGTACTCTGAGCCTCGCCATTGGGCACTGTTAATCTCACCCGTAATCTGTA	4437
Qy	4418	ATTGAGTGTATATCAATTAACCGGTTAATTCGTGCAGTTGAACCTTGATCATGTCTCT	4477
Db	4435	ATTGATATTATTAATCAATTAACCGGTTGATTTGTTCAAGTTAACTTTGGTCTCTGTGCT	4499
Qy	4478	TATTAATCTTAATCTGTGTCAACATAGCAACCGGTTACATTAATCTGATTGGCTTTCG	4537
Db	4495	TCTTAATCTTATC-GGTTTCCATAGCAACTGGTTACATTAATCTGATTGGGCGCTTCA	4555
Qy	4538	CGA-----ATACCCCTAGTATATGAGATTTGCCACTTCCCTCTAT	4575
Db	4554	CGATTAAGAACATGACGTACACCGCGTAACTCCCTATGATGATGAGATTTGGCACTCCCTAT	4613
Qy	4576	GCGGCGCTGCTCGCTCGGTTGGGCGCGGACAGACAGAGCTTGCCGTCGCGGACCTTTGG	4639
Db	4614	GCGGCTGCTCGCTCGGTTGGGCGCTCGGACCAAAGTCCGACAGACGCGAGAGCTCTGC	4673
Qy	4636	TCCGCGAGCCCGACCGAGCGACGCGCATATGAGGAGTGGCCAA	4683
Db	4674	TCTGCCGCGCCCGACCGAGCGAGCGCGCATATGAGGAGTGGCCAA	4721
RESULT 15			
ADV67509	ADV67509 standard; DNA; 4721 BP.		
XX	AC	ADV67509;	
XX	DT	10-MAR-2005 (first entry)	
XX	DE	Nucleotide sequence of AAV serotype 7.	
XX	KM	antiarteriosclerotic; antilipemic; gene therapy; cholesterol;	
KW	apolipoprotein E; apoE; apolipoprotein A; apoA; atherosclerosis;		
XX	lipoprotein defect; ss.		
OS	Adeno-associated virus.		
XX	Key	Location/Qualifiers	
EH	repeat_region	1..107	
FT		/tag= a	
FT		/note= "5' ITR"	
FT	misc_feature	825..3049	
FT		/tag= b	
FT		/note= "encodes vp1"	
FT	misc_feature	1234..3049	
FT		/tag= c	
FT		/note= "encodes vp2"	
FT	misc_feature	1434..3049	
FT		/tag= d	
FT		/note= "encodes vp3"	
FT	repeat_region	4704..4721	
FT		/tag= e	
FT		/note= "3' ITR"	
XX	PN	MO2004108922-A2.	
XX	PD	16-DEC-2004.	
XX			

PF 23-APR-2004; 2004MO-US010965.
XX
PR 25-APR-2003; 2003US-0465293P.
XX
PA (UVE-) UNIV PENNSYLVANIA.
XX
PI Rader DJ, Wilson JM,
XX
DR WPI; 2005-031700/03.
XX
PT Lowering total cholesterol levels and treating atherosclerosis in a
PT subject comprises delivering a recombinant adeno-associated virus (AAV)
PT comprising an AAV serotype capsid protein or a gene encoding human
PT apolipoprotein E (apoE) or apoA.
XX
PS Disclosure; SEQ ID NO 7; 69pp; English.
XX
CC The specification describes a method for lowering total cholesterol
CC levels in a subject. The method comprises delivering to the subject a
CC recombinant adeno-associated virus (AAV) comprising a gene encoding a
CC human apolipoprotein E (apoE) or apoA under the control of a regulatory
CC control sequence which directs expression of the gene. The recombinant
CC AAV also comprises a capsid protein selected from an AAV serotype (e.g.,
CC AAV7 or AAV8) which preferentially expresses high levels of transgene in
CC live. A therapeutically effective amount of apoE or apoA expression is
CC obtained upon delivery of low dose of AAV. The method of the invention is
CC useful for lowering total cholesterol levels in a subject, e.g. for
CC treating atherosclerosis, and for correcting defects in lipoprotein. The
CC present sequence represents AAV serotype 7 (AAV7), which may be used to
CC produce recombinant AAV vectors of the invention.
XX
SQ Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
Query Match 78.5%; Score 3678.4; DB 14; Length 4721;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 4135; Conservative 0; Mismatches 541; Indels 52; Gaps 8;
QY 1 TTGGCACTCCCTCTGCGGCTCGCTCGCTCACTGAGCGCGGCGCAACAAAGTCCGC 60
Db 1 TTGGCACTCCCTCTGCGGCTCGCTCGCTCGCTCGGTTGGGCTCGCGACCAAGTCCGC 60
QY 61 CGACGCCCGGGCTTTGCCGGGGCGGCTCACTGAGCGAGCGCGCGAGAGGAGTG 120
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QY 224 ACATTTTGGCAACCATGTGTGTCAGCTGGGTATTAAAGCCGAGTGAACGACGAGGTC 283
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Job time : 2697 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_env: *
2: gb_pat: *
3: gb_ph: *
4: gb_pl: *
5: gb_pr: *
6: gb_ro: *
7: gb_sts: *
8: gb_sy: *
9: gb_un: *
10: gb_vl: *
11: gb_ov: *
12: gb_htg: *
13: gb_in: *
14: gb_om: *
15: gb_da: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	4683	100.0	4683	2 BD242775 Adeno-ss
2	4683	100.0	4683	2 AR562507 Sequence
3	4683	99.6	4683	10 AF028704 Adeno-ss
4	4253.2	90.8	4718	2 BD242766 Adeno-ss
5	4253.2	90.8	4718	2 AR562498 Sequence
6	4253.2	90.8	4718	2 AX753251 Sequence
7	4253.2	90.8	4718	10 AF063497 Adeno-ss
8	3678.4	78.5	4721	2 CO972062 Sequence
9	3678.4	78.5	4721	2 CS073592 Sequence
10	3678.4	78.5	4721	2 AX753246 Sequence
11	3678.4	78.5	4721	10 AF513851 Adeno-ss
12	3404.6	72.0	4385	2 AX753250 Sequence
13	3370.4	72.0	4393	2 CO972063 Sequence
14	3370.4	72.0	4393	2 CS073594 Sequence
15	3370.4	72.0	4393	2 AX753249 Sequence
16	3370.4	70.4	4393	10 AF513852 Adeno-ss
17	3296.2	70.4	4679	2 AR762859 Sequence
18	3296.2	70.4	4679	2 AX282480 Sequence

19	3296.2	70.4	4679	10 AF043303 Adeno-ss
20	3296.2	70.4	8698	2 AR222044 Sequence
21	3296.2	70.4	8698	2 AX205072 Sequence
22	3270.8	69.8	4680	2 AR028767 Sequence
23	3270.8	69.8	4680	2 I62303 Sequence 1
24	3267.8	69.8	4681	2 BD242774 Adeno-ss
25	3267.8	69.8	4681	2 AR562506 Sequence
26	3255.4	69.5	4102	10 AR631965 Adeno-ss
27	3244.2	69.3	4675	2 BD094552 Method of
28	3244.2	69.3	4675	2 AR697188 Sequence
29	3244.2	69.3	4675	2 AR697189 Sequence
30	3244.2	69.3	4675	2 AX135805 Sequence
31	3244.2	69.3	4675	2 AX286292 Sequence
32	3244.2	69.3	4675	2 AX753252 Sequence
33	3244.2	69.3	4675	10 AA2CG
34	3182.8	68.0	4722	10 AF028705 Adeno-ss
35	3149	67.2	4726	2 AX753253 Sequence
36	3149	67.2	4726	10 AVU48704 Adeno-ss
37	3114.4	66.5	7557	2 AR222045 Sequence
38	3114.4	66.5	7557	2 AX205073 Sequence
39	3106.6	66.3	4430	10 AY695374 Adeno-ss
40	3106.4	66.3	4429	10 AY695375 Adeno-ss
41	3101.6	66.2	4429	10 AY695372 Adeno-ss
42	3100	66.2	4429	10 AY695371 Adeno-ss
43	3098.4	66.2	4429	10 AY695373 Adeno-ss
44	3089	66.0	4430	10 AY695376 Adeno-ss
45	3008	64.2	8179	2 BD271148 Virus vec

ALIGNMENTS

RESULT 1	BD242775	4683 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	Adeno-ss-associated virus serum type 1	nucleic acid sequence, vector			
DEFINITION	Adeno-ss-associated virus serum type 1	nucleic acid sequence, vector			
ACCESSION	BD242775				
VERSION	BD242775.1	GI:33052545			
KEYWORDS	UP 2002529098-A/10.				
SOURCE	unidentified				
ORGANISM	unclassified sequences.				
REFERENCE	1 (bases 1 to 4683)				
AUTHORS	Wilson, J.M. and Xiao, W.				
TITLE	Adeno-ss-associated virus serum type 1 nucleic acid sequence, vector				
JOURNAL	Adeno-ss-associated virus serum type 1 nucleic acid sequence, vector				
COMMENT	Patent: JP 2002529098-A 10 10-SEP-2002; THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA				
OS	aav-6				
PN	JP 2002529098-A/10				
PD	10-SEP-2002				
PR	02-NOV-1999 JP 2000581227				
PI	05-NOV-1998 US 60/107114				
PC	JAMES M WILSON, WEIDONG XIAO				
CC	C12N15/09, A61K31/711, A61K48/00, A61P43/00, C12N1/15, C12N1/19, PC				
FT	1. .4683				
FT	location/Qualifiers				
FT	source				
FEATURES	location/Qualifiers				
source	1. .4683				
ORIGIN	/organism="unidentified"				
ORIGIN	/mol_type="genomic DNA"				
ORIGIN	/db_xref="taxon:32644"				
Query Match	100.0%; Score 4683; DB 2; Length 4683;				
Best Local Similarity	100.0%; Pred. No. 0;				

Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAAGGCCGGGCGCAACCAAGGTGCC	60	
Db	1	TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAAGGCCGGGCGCAACCAAGGTGCC	60	
Qy	61	CGACGCCGGGCTTTGCCCGGGCGGCTCAGTGAAGCAGAGCGGCGCAGAGAGGAGTG	120	
Db	61	CGACGCCGGGCTTTGCCCGGGCGGCTCAGTGAAGCAGAGCGGCGCAGAGAGGAGTG	120	
Qy	121	GCCAACTCCACTACTAGGGGTTCTTGAGAGGGTGAAGTCTGACGTGAATTAAGTCAATAG	180	
Db	121	GCCAACTCCACTACTAGGGGTTCTTGAGAGGGTGAAGTCTGACGTGAATTAAGTCAATAG	180	
Qy	181	GGTTAAGGAGTCTCTGTATTAAGAGTCAAGTGAATTTTGGCAATTTTGGCAGCAT	240	
Db	181	GGTTAAGGAGTCTCTGTATTAAGAGTCAAGTGAATTTTGGCAATTTTGGCAGCAT	240	
Qy	241	GTGGTCAAGCTGAGTATTTAAAGCCGAGTGAACAGAGAGTCTCAATTTTGAAGCGGGA	300	
Db	241	GTGGTCAAGCTGAGTATTTAAAGCCGAGTGAACAGAGAGTCTCAATTTTGAAGCGGGA	300	
Qy	301	GGTTGAACGCGCAGCGCCATGCGGGGTTTACGAGATTGTATTAAGTCCCACGGA	360	
Db	301	GGTTGAACGCGCAGCGCCATGCGGGGTTTACGAGATTGTATTAAGTCCCACGGA	360	
Qy	361	CTTTGAGAGAGATGCGCCGSCATTTCTGACAGCTTTTGAACTGGGAGCGGAGGA	420	
Db	361	CTTTGAGAGAGATGCGCCGSCATTTCTGACAGCTTTTGAACTGGGAGCGGAGGA	420	
Qy	421	ATGGAGATTGCGCGCAGATTCTGACATGATCTGAACTGAATTGAGAGGACCCCTGAC	480	
Db	421	ATGGAGATTGCGCGCAGATTCTGACATGATCTGAACTGAATTGAGAGGACCCCTGAC	480	
Qy	481	CGTGGCGGAGAAAGTGCAGCGCGACTTCCTGTCTCACTGCGCGCGCTGAAGTACGCC	540	
Db	481	CGTGGCGGAGAAAGTGCAGCGCGACTTCCTGTCTCACTGCGCGCGCTGAAGTACGCC	540	
Qy	541	GGAGGCCCTCTTCTTTGTCAGTTGCGAAGAGGAGGAGTCCACTCAACCTCCATTTCT	600	
Db	541	GGAGGCCCTCTTCTTTGTCAGTTGCGAAGAGGAGGAGTCCACTCAACCTCCATTTCT	600	
Qy	601	GGTGGAGACCAAGGGGCTCAATCCATGTGCTGAGCGCTTCCCTGAGTCAGATTAGCGA	660	
Db	601	GGTGGAGACCAAGGGGCTCAATCCATGTGCTGAGCGCTTCCCTGAGTCAGATTAGCGA	660	
Qy	661	CAAGCTGTGCAACCATCTACCGCGGAGTGAAGCCGACCTGCGCAACTGTGTCGGGT	720	
Db	661	CAAGCTGTGCAACCATCTACCGCGGAGTGAAGCCGACCTGCGCAACTGTGTCGGGT	720	
Qy	721	GACCAAGCGGTAAATGGCGCGGAGGGGGGAAACAAGTGTGAGCAGATCTACATCCC	780	
Db	721	GACCAAGCGGTAAATGGCGCGGAGGGGGGAAACAAGTGTGAGCAGATCTACATCCC	780	
Qy	781	CAACTACTCTGCGCAAGACTCAGCGGAGCTGAGTGGCGTGAATTAAGTGAAGA	840	
Db	781	CAACTACTCTGCGCAAGACTCAGCGGAGCTGAGTGGCGTGAATTAAGTGAAGA	840	
Qy	841	GTATATAAGCGGTGTTAACTTGGCGGAGCGCAAAAGCTGTGGCGCAGACTGAC	900	
Db	841	GTATATAAGCGGTGTTAACTTGGCGGAGCGCAAAAGCTGTGGCGCAGACTGAC	900	
Qy	901	CCAGTCAAGCGGAGCCGAGAGCAAGCAAGAGAACTGAACCCCAATTTGACGGGCC	960	
Db	901	CCAGTCAAGCGGAGCCGAGAGCAAGCAAGAGAACTGAACCCCAATTTGACGGGCC	960	
Qy	961	TGTATCCGCTCAAAAACCTTCGACGCTACATGAGCTGTGCGGTGCTGTGACCG	1020	
Db	961	TGTATCCGCTCAAAAACCTTCGACGCTACATGAGCTGTGCGGTGCTGTGACCG	1020	
Qy	1021	GGGATCACTCTCGGAGAAAGAGTGAATCAGAGAGACCAAGGCTCTGTACATCTCTTCAA	1080	
Db	1021	GGGATCACTCTCGGAGAAAGAGTGAATCAGAGAGACCAAGGCTCTGTACATCTCTTCAA	1080	

Qy	1081	CGCGGCTCCAACTCGGAGTCCAGATCAAGGCGCTGTGACAAATGCGGCAAGATCAT	1140	
Db	1081	CGCGGCTCCAACTCGGAGTCCAGATCAAGGCGCTGTGACAAATGCGGCAAGATCAT	1140	
Qy	1141	GGCGTGAACCAATTCGCGCGCGACTACTGTAGGCCCGCTCCGCGCGGACATTTAA	1200	
Db	1141	GGCGTGAACCAATTCGCGCGCGACTACTGTAGGCCCGCTCCGCGCGGACATTTAA	1200	
Qy	1201	AACCAACCGATTTTACCGATCTCTGAGAGTGAACGAGTCAAGCTGAGTGGCTC	1260	
Db	1201	AACCAACCGATTTTACCGATCTCTGAGAGTGAACGAGTCAAGCTGAGTGGCTC	1260	
Qy	1261	CGCTTTCTCGGCTGGGCGCAGAAAGGTTGAGAAAACGCAACCATCTGCTGTTGG	1320	
Db	1261	CGCTTTCTCGGCTGGGCGCAGAAAGGTTGAGAAAACGCAACCATCTGCTGTTGG	1320	
Qy	1321	GCCGCGCACAGGGCAAGACCAATCGGGAAGCCATGCGCCAGCGGCTCTTCTA	1380	
Db	1321	GCCGCGCACAGGGCAAGACCAATCGGGAAGCCATGCGCCAGCGGCTCTTCTA	1380	
Qy	1381	CGGCTGCTCAACTGGAACCAATGAACCTTCCCTTCAAGATTTGGTGAAGATGCT	1440	
Db	1381	CGGCTGCTCAACTGGAACCAATGAACCTTCCCTTCAAGATTTGGTGAAGATGCT	1440	
Qy	1441	GATCTGGGAGAGGAGCAAGATGACGCGCAAGTCTGTGAGTCCGCCAAGGCCATTCT	1500	
Db	1441	GATCTGGGAGAGGAGCAAGATGACGCGCAAGTCTGTGAGTCCGCCAAGGCCATTCT	1500	
Qy	1501	CGGCGGAGAGAGTGGCGCTGGAACCAAAATGCAAGTCTCCGCCAGATCCAC	1560	
Db	1501	CGGCGGAGAGAGTGGCGCTGGAACCAAAATGCAAGTCTCCGCCAGATCCAC	1560	
Qy	1561	CCCCGTGATGTAACCTCCAAACCAATGTCGCGCTGATGAGGGGAGACGACAC	1620	
Db	1561	CCCCGTGATGTAACCTCCAAACCAATGTCGCGCTGATGAGGGGAGACGACAC	1620	
Qy	1621	CTTCAAGACCAAGCGGTTGACGACCGGATGTTCAATTTGAATCTCACCCGCGTCT	1680	
Db	1621	CTTCAAGACCAAGCGGTTGACGACCGGATGTTCAATTTGAATCTCACCCGCGTCT	1680	
Qy	1681	GAGCATGACTTTGGCAAGGTGACAAAGCAGAGTCTCAAGTCTTCCGCTGGGCGCA	1740	
Db	1681	GAGCATGACTTTGGCAAGGTGACAAAGCAGAGTCTCAAGTCTTCCGCTGGGCGCA	1740	
Qy	1741	GGATCAAGTGAACGAGGTGCGATGAGTCTAAGTCAAGAAAGGTGAGCCAAACAG	1800	
Db	1741	GGATCAAGTGAACGAGGTGCGATGAGTCTAAGTCAAGAAAGGTGAGCCAAACAG	1800	
Qy	1801	ACCGGCGCGGATGACGCGGATAAAGCGAGCCCAAGCGGCGCTCAAGTCGCGGA	1860	
Db	1801	ACCGGCGCGGATGACGCGGATAAAGCGAGCCCAAGCGGCGCTCAAGTCGCGGA	1860	
Qy	1861	TCAATGAGCTCAAGCGGAGAGGCTCGGTGAGACTTTGCGGACAGATCCAAACAA	1920	
Db	1861	TCAATGAGCTCAAGCGGAGAGGCTCGGTGAGACTTTGCGGACAGATCCAAACAA	1920	
Qy	1921	ATGTTCTGTCAGCGGCGGATGCTTCAAGTGTGTTTCCCTGCAAAACATGAGGAAT	1980	
Db	1921	ATGTTCTGTCAGCGGCGGATGCTTCAAGTGTGTTTCCCTGCAAAACATGAGGAAT	1980	
Qy	1981	GAATCAGAAATTTCAACATTTTCTTCAACGCGGACAGAGACTGTTTCAAGATGTTCCC	2040	
Db	1981	GAATCAGAAATTTCAACATTTTCTTCAACGCGGACAGAGACTGTTTCAAGATGTTCCC	2040	
Qy	2041	CGGCTGTCAAGAACTTCAACCGGCTGTGAGAAAGAGACGTATTCGAAATCTGTGCTAT	2100	
Db	2041	CGGCTGTCAAGAACTTCAACCGGCTGTGAGAAAGAGACGTATTCGAAATCTGTGCTAT	2100	
Qy	2101	TCAATCATCTGCGGCGGCTCCAGAGATGCTTGTGCGGCTCGGATCTGTGCAAGCT	2160	
Db	2101	TCAATCATCTGCGGCGGCTCCAGAGATGCTTGTGCGGCTCGGATCTGTGCAAGCT	2160	

QY	2161	GGATCTCGATGACCTGTGTTTCTTGAGCAATAATGACTTAAACACAGTATGCTGCCGATG	2222
Db	2161	GGATCTGGAATGACTGTGTGTTTCTGAGCAATAATGACTTAAATGACTTAAACACAGTATGCTGCCGATG	2222
QY	2221	GTTATCTTCCAAATTGGGCTCGAGGACAACCTCTCGAGGGGCAATTGGGGAGTGGTGGAGACT	2288
Db	2221	GTTATCTTCCAAATTGGGCTCGAGGACAACCTCTCGAGGGGCAATTGGGGAGTGGTGGAGACT	2288
QY	2281	TGAAAACCTGAGACCCCGAAAACCCAAAGCCCAACAGCAAAAGCAGAGCGACGACCGGGGTCT	2340
Db	2281	TGAAAACCTGAGACCCCGAAAACCCAAAGCCCAACAGCAAAAGCAGAGCGACGACCGGGGTCT	2340
QY	2341	TGTCGCTTCTCGGCTTAACAATGACTCTTCGGAACCTTCAACAAGGACTCGACAAGGGGGAGCCCG	2400
Db	2341	TGTCGCTTCTCGGCTTAACAATGACTCTTCGGAACCTTCAACAAGGACTCGACAAGGGGGAGCCCG	2400
QY	2401	TCAAAGCGCGGCAATGACAGCGGCTCGAGCAAGACAGGCGCTTAACAAGGACTCGACAAG	2460
Db	2401	TCAAAGCGCGGCAATGACAGCGGCTCGAGCAAGACAGGCGCTTAACAAGGACTCGACAAG	2460
QY	2461	CGGGTGAACAATCGTACCTGCGGTATTAACAAGCGGACGCGCGAGTTTTCAGAGCGCTTCGAC	2520
Db	2461	CGGGTGAACAATCGTACCTGCGGTATTAACAAGCGGACGCGCGAGTTTTCAGAGCGCTTCGAC	2520
QY	2521	AAGAAAGATACGCTTTTGGGGGCAACCTCGGGCGAGCAAGCTTTCAGGCGCAAGAAAGAGGG	2580
Db	2521	AAGAAAGATACGCTTTTGGGGGCAACCTCGGGCGAGCAAGCTTTCAGGCGCAAGAAAGAGGG	2580
QY	2581	TTCTCGAACTTTTGGGTCTGGTTGAGGAAGTGTCTAACAAGGCTCTTGGAAGAAACGCTC	2640
Db	2581	TTCTCGAACTTTTGGGTCTGGTTGAGGAAGTGTCTAACAAGGCTCTTGGAAGAAACGCTC	2640
QY	2641	CGGTGAGACAGTCGCGCACAAAGAGCCAGACTCTCTCGGGGCAATTGGGCAAGACAGGCGACG	2700
Db	2641	CGGTGAGACAGTCGCGCACAAAGAGCCAGACTCTCTCGGGGCAATTGGGCAAGACAGGCGACG	2700
QY	2701	AGCCCGCTAATAAAGAAGACTCAATTTTGGTCAAGCTGGCGACTCAAGGTCAGTCCCGAAC	2760
Db	2701	AGCCCGCTAATAAAGAAGACTCAATTTTGGTCAAGCTGGCGACTCAAGGTCAGTCCCGAAC	2760
QY	2761	CACAACTCTCGGABAACTCTCAAGAACCCCGCGCTGTGGGACTCTCAACAAAGGCTT	2820
Db	2761	CACAACTCTCGGABAACTCTCAAGAACCCCGCGCTGTGGGACTCTCAACAAAGGCTT	2820
QY	2821	CAGGCGGTGCGCACCAATGAGCACAATTAAGAAAGCGCGCAGAGTGGGTAAATGCTT	2880
Db	2821	CAGGCGGTGCGCACCAATGAGCACAATTAAGAAAGCGCGCAGAGTGGGTAAATGCTT	2880
QY	2881	CAGGAAATTGGCATTTGCGATTTCCACATGGCTGGGCGACAGAGTCAACAACAGCACCC	2940
Db	2881	CAGGAAATTGGCATTTGCGATTTCCACATGGCTGGGCGACAGAGTCAACAACAGCACCC	2940
QY	2941	GAACTATGGGCTTTGGCCCACTTAAACAACCTTAACAAGCAATTCACAGTGGCTTCA	3000
Db	2941	GAACTATGGGCTTTGGCCCACTTAAACAACCTTAACAAGCAATTCACAGTGGCTTCA	3000
QY	3001	CGGGGGCGAGCAAGCAACAACCTACTTGGCTACAGCACCCCGGGGGGTATTTTGAAT	3060
Db	3001	CGGGGGCGAGCAAGCAACAACCTACTTGGCTACAGCACCCCGGGGGGTATTTTGAAT	3060
QY	3061	TCACAGATTCACCTGCGATTTCTCAACAAGTGAAGCTGACAGGACTCAACAACAAT	3120
Db	3061	TCACAGATTCACCTGCGATTTCTCAACAAGTGAAGCTGACAGGACTCAACAACAAT	3120
QY	3121	GGGGAATTCGGGCTCAAGAGCTCAACTTCAGCTCTTCAACATTCGAAGTCAAGAGGCTCA	3180
Db	3121	GGGGAATTCGGGCTCAAGAGCTCAACTTCAGCTCTTCAACATTCGAAGTCAAGAGGCTCA	3180
QY	3181	CGACCAATGATGGGCTCAAGACCAATCGGCTAATTAACCTTAACAAGCGGTTCAAGTCTGT	3240
Db	3181	CGACCAATGATGGGCTCAAGACCAATCGGCTAATTAACCTTAACAAGCGGTTCAAGTCTGT	3240
QY	3241	CGGACTCGGAATACAGATTTCCGTAAGTCTTCGAGCTTGGCGACCAAGGGCTGCTCCTCT	3300

Db	3241	CGAGTCGGAGATACCAAGTTCCCGAAGCTTCGAGCTCGCGACACAGGCGCTCCCTC	3300
QY	3301	CGTTCCCGGCGAGCGTGTTCATGATTCGCGAGTACGAGCTACCTAAACGCTCAACATGGCA	3360
Db	3301	CGTTCCCGGCGAGCGTGTTCATGATTCGCGAGTACGAGCTACCTAAACGCTCAACATGGCA	3360
QY	3361	GCCAGGCAGTGGGACGCTCATCTCTTTTACCTGCGAAATATTTCCCATCGAGATGCTGA	3420
Db	3361	GCCAGGCAGTGGGACGCTCATCTCTTTTACCTGCGAAATATTTCCCATCGAGATGCTGA	3420
QY	3421	GAA CGGGCAATTAACCTTACCTTCAGCTACACTTCGAGAGCGTCCCTTCCACAGCAAGCT	3480
Db	3421	GAA CGGGCAATTAACCTTACCTTCAGCTACACTTCGAGAGCGTCCCTTCCACAGCAAGCT	3480
QY	3481	AACGCGACAGCGAGAGCTTGACCGGCGTGAATGATTCCTCATGCAACCACTAGCTATTT	3540
Db	3481	AACGCGCGACAGCGAGAGCTTGACCGGCGTGAATGATTCCTCATGCAACCACTAGCTATTT	3540
QY	3541	AACCTGAACAGAACTCAACATCAGTCCGGAAGTGCCCAAAACAGAGACTTGTGTTTACCC	3600
Db	3541	AACCTGAACAGAACTCAACATCAGTCCGGAAGTGCCCAAAACAGAGACTTGTGTTTACCC	3600
QY	3601	GTGGGTCTCCAGCTGGGCAATGTCTGTTCAGCCCAAAACTGGCTACGTGAGACCTGTATAC	3660
Db	3601	GTGGGTCTCCAGCTGGGCAATGTCTGTTCAGCCCAAAACTGGCTACGTGAGACCTGTATAC	3660
QY	3661	GGCAGCAGCGGTTTCTTAAACAAAAAACAGCAACAACAGAGACTTTCCTGAGACTG	3720
Db	3661	GGCAGCAGCGGTTTCTTAAACAAAAAACAGCAACAACAGAGACTTTCCTGAGACTG	3720
QY	3721	GTGCTTCAAAATATTAACCTTAATGGGCGTGAATCTATTAATCAACCTTGAGCACTGTAG	3780
Db	3721	GTGCTTCAAAATATTAACCTTAATGGGCGTGAATCTATTAATCAACCTTGAGCACTGTAG	3780
QY	3781	CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGCATGATTTTTGGAA	3840
Db	3781	CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGCATGATTTTTGGAA	3840
QY	3841	AGGAGAGCGCGGAGCTTCAAAACACTGACATTGACCAATGTCATATACACACGAGAGAG	3900
Db	3841	AGGAGAGCGCGGAGCTTCAAAACACTGACATTGACCAATGTCATATACACACGAGAGAG	3900
QY	3901	AAATCAAAAGCCATTAACCCCGTGGCCACCGAAGATTGGACTGTGGCACTCAATCTC	3960
Db	3901	AAATCAAAAGCCATTAACCCCGTGGCCACCGAAGATTGGACTGTGGCACTCAATCTC	3960
QY	3961	AGAGACGACGACAGACCCTGCGAACCGAGATGTGCATGTTATGGAGCCTTAACTTGAA	4020
Db	3961	AGAGACGACGACAGACCCTGCGAACCGAGATGTGCATGTTATGGAGCCTTAACTTGAA	4020
QY	4021	TGGTGTGCGCAAGACAGAGACGTATTAACCTGACGGGTCCATTTTGGGCGAAATTCCTCA	4080
Db	4021	TGGTGTGCGCAAGACAGAGACGTATTAACCTGACGGGTCCATTTTGGGCGCAAAATTCCTCA	4080
QY	4081	CGGATGGAACATTTCAACCCGCTCTCTCTCAATGGGCGGCTTTGGACTTAAGACACCGCCTC	4140
Db	4081	CGGATGGAACATTTCAACCCGCTCTCTCTCAATGGGCGGCTTTGGACTTAAGACACCGCCTC	4140
QY	4141	CTCAGATCTCATCAAAAACAGCGCTGTCTCTGCGAAATCCCGGCGAGAGTTTCGGCTA	4200
Db	4141	CTCAGATCTCATCAAAAACAGCGCTGTCTCTGCGAAATCCCGGCGAGAGTTTCGGCTA	4200
QY	4201	CAAAGTTTGCCTTCACTTATCAACCAAGATTTCCACAGACAAGTGAAGGTGAGATTAAT	4260
Db	4201	CAAAGTTTGCCTTCACTTATCAACCAAGATTTCCACAGACAAGTGAAGGTGAGATTAAT	4260
QY	4261	GGAGAGCTGCAAAAAGAAAACAGCAAAACGCTGGAATCCCGAAGTCCAGTATACATCTAAT	4320
Db	4261	GGAGAGCTGCAAAAAGAAAACAGCAAAACGCTGGAATCCCGAAGTCCAGTATACATCTAAT	4320
QY	4321	ATGCAAAATCTGCAACGTTGATTTCACTGTGACAAACATGACCTTTATCTGAGCTTC	4380

Db 1381 CCGGCTGTCACTGGACCAATGAGAACTTTCCCTTCAACGATTCGTCGACAAATGAT 1440
Qy 1441 GATCTGGGGAGGAGGCAAGATGACGGCCAAAGTCGAGATCGGCGCAAGGCCATTCT 1500
Db 1441 GATCTGGGGAGGAGGCAAGATGACGGCCAAAGTCGAGATCGGCGCAAGGCCATTCT 1500
Qy 1501 CCGGCGGCAAGAGTGCGCGTGGACCAAAAGTGAAGTCGTCGCCCGCATGATCCGAC 1560
Db 1501 CCGGCGGCAAGAGTGCGCGTGGACCAAAAGTGAAGTCGTCGCCCGCATGATCCGAC 1560
Qy 1561 CCCCCTGATCGTCACTCCAAACCAACATGTCGCCCTGATTTGACGGGAAACAGACAC 1620
Db 1561 CCCCCTGATCGTCACTCCAAACCAACATGTCGCCCTGATTTGACGGGAAACAGACAC 1620
Qy 1621 CTTGGAGACCAAGGCGCGTTGGACGAGACCGAATGTTCAAAATTTGAATCACCCCGCT 1680
Db 1621 CTTGGAGACCAAGGCGCGTTGGACGAGACCGAATGTTCAAAATTTGAATCACCCCGCT 1680
Qy 1681 GGAGCATGACTTTGGCAAGTGAACAAAGCAGAAATCAAGATTTCTCCGTCGGGCGCA 1740
Db 1681 GGAGCATGACTTTGGCAAGTGAACAAAGCAGAAATCAAGATTTCTCCGTCGGGCGCA 1740
Qy 1741 GGATCACTGAACCGAGTGGCGCATGAGTTCTTACGTCAGAAAGGCTGACCAACAG 1800
Db 1741 GGATCACTGAACCGAGTGGCGCATGAGTTCTTACGTCAGAAAGGCTGACCAACAG 1800
Qy 1801 ACCCGCCCCGATGACGGGGATPAAAAGGAGCCGAGGGCGCTGCCCTCAGTCGCGGA 1860
Db 1801 ACCCGCCCCGATGACGGGGATPAAAAGGAGCCGAGGGCGCTGCCCTCAGTCGCGGA 1860
Qy 1861 TCCATCGACGTCAAGACGGGAAGAGCTCCGGTGAATTTGCCGACAGTACCAAAACA 1920
Db 1861 TCCATCGACGTCAAGACGGGAAGAGCTCCGGTGAATTTGCCGACAGTACCAAAACA 1920
Qy 1921 ATGTTCTGTCACCGGGGATGCTTCAAGTCTGTTTCCCTGCAAAACATCGAGAGAT 1980
Db 1921 ATGTTCTGTCACCGGGGATGCTTCAAGTCTGTTTCCCTGCAAAACATCGAGAGAT 1980
Qy 1981 GAATCAGAAATTTCAACATTTGCTTCAAGCAGGACCGAGACGTTGAGAAATGTTTCCC 2040
Db 1981 GAATCAGAAATTTCAACATTTGCTTCAAGCAGGACCGAGACGTTGAGAAATGTTTCCC 2040
Qy 2041 CCGGCTGTCAAGATCTCAACCGGTGTGAGAAAGAGAGTATCGGAAATCTGTGCCAT 2100
Db 2041 CCGGCTGTCAAGATCTCAACCGGTGTGAGAAAGAGAGTATCGGAAATCTGTGCCAT 2100
Qy 2101 TCATCATCTGCTGGGGCGGGCTCCCGAATTTGCTTGTGCGCTGCGATCTGATCAAGT 2160
Db 2101 TCATCATCTGCTGGGGCGGGCTCCCGAATTTGCTTGTGCGCTGCGATCTGATCAAGT 2160
Qy 2161 GGATCTGGATGACGTGTGTTTCTGAGCAATAATGACTTTAAACAGGTAATGCTGCCATG 2220
Db 2161 GGATCTGGATGACGTGTGTTTCTGAGCAATAATGACTTTAAACAGGTAATGCTGCCATG 2220
Qy 2221 GTTATCTTCCAGATTGGCTCGAGGACCAACTCTGAGGGCAATTCGAGAGTGGTGGAGCT 2280
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VERSION AF028704.1 GI:2766605
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SOURCE Adeno-associated virus 6
ORGANISM Adeno-associated virus 6
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Rutledge, E.A., Halbert, C.L. and Russell, D.W.
Infectious clones and vectors derived from adeno-associated virus
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J. Virol. 72 (1), 309-319 (1998)
JOURNAL 9420229
PUBMED 2 (bases 1 to 4683)
REFERENCE Rutledge, E.A. and Russell, D.W.
Direct Submission
Submitted (24-SEP-1997) Hematology, Univ. of Washington, Box
357720, Seattle, WA 98195, USA
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Query Match

99.6%; Score 4663.8; DB 10; Length 4683;

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QY 3661 GGCAGAGCGCGCTTCTTAAACAAACAAACAGCAACAAACAGCAACTTATCTGAGCTG 3720
DB 3661 GGCAGAGCGCGCTTCTTAAACAAACAAACAGCAACAAACAGCAACTTATCTGAGCTG 3720
QY 3721 GTGCTTCAAAATATTAATCTTATGAGGCGTGAATCTATATCAACCTGAGCACTGATGG 3780
DB 3721 GTGCTTCAAAATATTAATCTTATGAGGCGTGAATCTATATCAACCTGAGCACTGATGG 3780
QY 3781 CCTCACAACAAAGAGCAACAAAGCAAGTCTTCTCCATGAGCGGATGATGATTTTGGAA 3840
DB 3781 CCTCACAACAAAGAGCAACAAAGCAAGTCTTCTCCATGAGCGGATGATGATTTTGGAA 3840
QY 3841 AGGAGAGCGCGGAGCTTCAACCACTGCAATTGACAAATGTCATGATCAAGAGAGAGG 3900
DB 3841 AGGAGAGCGCGGAGCTTCAACCACTGCAATTGACAAATGTCATGATCAAGAGAGAGG 3900
QY 3901 AAATCAAGGCACTAATCCCGTGGCCACCGAAAGATTTGGGACTGTGGCACTGTCC 3960
DB 3901 AAATCAAGGCACTAATCCCGTGGCCACCGAAAGATTTGGGACTGTGGCACTGTCC 3960
QY 3961 AGAGCAGCAGCAGACCTTGCAGCGGAGATGTGATGTTATGGAGCTTACCTGGAA 4020
DB 3961 AGAGCAGCAGCAGACCTTGCAGCGGAGATGTGATGTTATGGAGCTTACCTGGAA 4020
QY 4021 TGGTGTGGCAAGACAGAGATGATCTGAGAGGCTCTATTTGGGCCAAATTCCTCACA 4080
DB 4021 TGGTGTGGCAAGACAGAGATGATCTGAGAGGCTCTATTTGGGCCAAATTCCTCACA 4080
QY 4081 CCGATGAGCACTTTCAACCCGCTCTCTCATGAGGCGGCTTTGACCTTAAACACCCGCTC 4140
DB 4081 CCGATGAGCACTTTCAACCCGCTCTCTCATGAGGCGGCTTTGACCTTAAACACCCGCTC 4140
QY 4141 CTCAGATCTCATCAATAAACAAGCGCTGTCTCGGAAATCTCTCCGGCAGAGTCTTCCGCTA 4200
DB 4141 CTCAGATCTCATCAATAAACAAGCGCTGTCTCGGAAATCTCTCCGGCAGAGTCTTCCGCTA 4200
QY 4201 CAAAGTTTGTCTTCAATCAACCAAGTATTCACAGAACAAAGTGAAGTGAAT 4260
DB 4201 CAAAGTTTGTCTTCAATCAACCAAGTATTCACAGAACAAAGTGAAGTGAAT 4260
QY 4261 GGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGGAAGTGAATATCTTAAT 4320
DB 4261 GGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGGAAGTGAATATCTTAAT 4320
QY 4321 ATGCAAAATCTGCCAAGTTGATTTCACTGTGACAACTTATTAATGAGGCTC 4380

OY 1123 CAATGCCGGAAGATCATGCGCTGACCAAAATCCGCGCCGACCTACCTGTAGGCCCCGC 1182
Db 1138 CAATGCCGGAAGATCATGCGCTGACCAAAATCCGCGCCGACCTACCTGTAGGCCCCGC 1197
OY 1183 TCCGCGCGGCAATTTAAACCAACCGCATTTTACCGCATCTTGAGCTGAAACGCTACGA 1242
Db 1198 TCCGCGCGGCAATTTAAACCAACCGCATTTTACCGCATCTTGAGCTGAAACGCTACGA 1257
OY 1243 CCGTCCCAACGCGCGCTCCGCTTTCTGCGCTGGGCCCCGAAAAGTTCCGAAAACGCA 1302
Db 1258 ACTGCTCAACGCGCGCTCCGCTTTCTGCGCTGGGCCCCGAAAAGTTCCGAAAACGCA 1317
OY 1303 CACCATCTGCGCTTTGCGCGCGGACCAACGCGGCAAGACCAACATCGCGAAGCCATCGC 1362
Db 1318 CACCATCTGCGCTTTGCGCGCGGACCAACGCGGCAAGACCAACATCGCGAAGCCATCGC 1377
OY 1363 CCAACGCGCTGCCCTTTCTACCGGCTGCTCACTGACCAATGAAAATTTCCTTCAACGA 1422
Db 1378 CCAACGCGCTGCCCTTTCTACCGGCTGCTCACTGACCAATGAAAATTTCCTTCAATGA 1437
OY 1423 TTGCGTCAAGATGATGATCTGGTTGGAGGAGGGAAGATGACGCGCAAGTCTGGA 1482
Db 1438 TTGCGTCAAGATGATGATCTGGTTGGAGGAGGGAAGATGACGCGCAAGTCTGGA 1497
OY 1483 GTCCGCAAGGCAATTTCTCGGCGGAGGCAAGTGGCGCTGACCAAAAGTCAAGTCGTC 1542
Db 1498 GTCCGCAAGGCAATTTCTCGGCGGAGCAAGTGGCGCTGAGCAAAAGTCAAGTCGTC 1557
OY 1543 CGCCCAAGTCCATCCCAACCCCGCTGATGTCACCTCCACCAACATGTCGCCCTGAT 1602
Db 1558 CGCCCAAGTCCACCCCAACCCCGCTGATGTCACCTCCACCAACATGTCGCCCTGAT 1617
OY 1603 TGAAGGGAACAGCAACCACTTGAAGCAACAGAGCGCTGAGAGCCGAGTTCAAATT 1662
Db 1618 TGAAGGGAACAGCAACCACTTGAAGCAACAGAGCGCTGAGAGCCGAGTTCAAATT 1677
OY 1663 TGAATCTCAACCGCGCTGAGAGCAATGCTTTGGCAAGGTGACAAAGAGGAAGTCAAGA 1722
Db 1678 TGAATCTCAACCGCGCTGAGAGCAATGCTTTGGCAAGGTGACAAAGAGGAAGTCAAGA 1737
OY 1723 GTTCTTCCGCTGGGCGCAAGATCATCTGACCGAGGTGCGCATGATTTCTACAGAA 1782
Db 1738 GTTCTTCCGCTGGGCGCAAGATCATCTGACCGAGGTGCGCATGATTTCTACAGAA 1797
OY 1783 GGGTGAAGCAACAAAGCAACCGCGCGGAGTGAAGCGGATTAAGCGAGCCCAAGCGGCG 1842
Db 1798 GGGTGAAGCAACAAAGCAACCGCGCGGAGTGAAGCGGATTAAGCGAGCCCAAGCGGCG 1857
OY 1843 CTGCCCCTCAAGTCGCGGATTCATTCAGCGTCAAGCGGAGAGAGCTCCGCTGATTTGC 1902
Db 1858 CTGCCCCTCAAGTCGCGGATTCATTCAGCGTCAAGCGGAGAGAGCTCCGCTGATTTGC 1917
OY 1903 CGACAGGTACCAAAACAAATGTTCTGCTACCGCGGCAATGCTTCAAGTCTGTTCCCTG 1962
Db 1918 CGACAGGTACCAAAACAAATGTTCTGCTACCGCGGCAATGCTTCAAGTCTGTTCCCTG 1977
OY 1963 CAAAACATGCGAGAGATGAATCAGATTTCAACATTTGCTTACAGCAAGGAGCCAGAGA 2022
Db 1978 CAAAACATGCGAGAGATGAATCAGATTTCAACATTTGCTTACAGCAAGGAGCCAGAGA 2037
OY 2023 CTGTTCAAGATGTTTCCCGGCGTGTCAAGATCTTCACCGGCTGTCAAGAAAGAGACTTA 2082
Db 2038 CTGTTCAAGATGTTTCCCGGCGTGTCAAGATCTTCACCGGCTGTCAAGAAAGAGACTTA 2097
OY 2083 TCGGAAATCTGTGCAATTCATCTGTGTGGGCGGCGCTCCGAGATTGCTGTCCGCG 2142
Db 2098 TCGGAAATCTGTGCAATTCATCTGTGTGGGCGGCGCTCCGAGATTGCTGTCCGCG 2157
OY 2143 CTGCAATCTGGTCAAGGTGATCTGAGATGATGATGTTCTGAGCAATTAAGACTTAAC 2202
Db 2158 CTGCAATCTGGTCAAGGTGATCTGAGATGATGATGTTCTGAGCAATTAAGACTTAAC 2217

OY 2203 CAGGTATGCTGCGCATGATTTATCTTCAGATTTGCTCGAGGACCAACTCTCTGAGGCA 2262
Db 2218 CAGGTATGCTGCGCATGATTTATCTTCAGATTTGCTCGAGGACCAACTCTCTGAGGCA 2277
OY 2263 TTGCGCATGTGTGGGACTTTGAAACTCTGAGACCCCGGAAACCCAAAGCCCAACGAGAAAGC 2322
Db 2278 TTGCGCATGTGTGGGACTTTGAAACTCTGAGACCCCGGAAAGCCCAAGCCCAACGAGAAAGC 2337
OY 2323 AGGACAGCGGCGGGGATCTGTGCTTCTGCTTCAAGATCTCGACCTTCGAAACGAGC 2382
Db 2338 AGGACAGCGGCGGGGATCTGTGCTTCTGCTTCAAGATCTCGACCTTCGAAACGAGC 2397
OY 2383 TCGACAAAGGAGAGCCCGCTCAACGCGCGGATGACGCGGCTTCGAGCAAGAGGCTT 2442
Db 2398 TCGACAAAGGAGAGCCCGCTCAACGCGCGGATGACGCGGCTTCGAGCAAGAGGCTT 2457
OY 2443 ACGACAGGAGCTTAAAGCGGCTGACATCCGTAACCTGCGGTATTAACAGCCGAGAGCCG 2502
Db 2458 ACGACAGGAGCTTAAAGCGGCTGACATCCGTAACCTGCGGTATTAACAGCCGAGAGCCG 2517
OY 2503 AGTTTCAAGAGCGCTGCTCAAGAGATACGCTTTTGGGGCAACCTCGGCGAGCAGTCT 2562
Db 2518 AGTTTCAAGAGCGCTGCTCAAGAGATACGCTTTTGGGGCAACCTCGGCGAGCAGTCT 2577
OY 2563 TCCAGGCAAGAGAGGCTTCTGAACTTTTGTGTTGAGAAAGTGTCTAAGACGG 2622
Db 2578 TCCAGGCAAGAGAGGCTTCTGAACTTTTGTGTTGAGAAAGGCTGTAAAGACGG 2637
OY 2623 CTCTGGAAGAAACCTTCGCTAGAGATGCGCAAGAGCCAGACTCTCTCCGCGCA 2682
Db 2638 CTCTGGAAGAAACCTTCGCTAGAGATGCGCAAGAGCCAGACTCTCTCCGCGCA 2697
OY 2683 TTGCGAAGAGGCGCAGCAGCCGCTTAAAGAGACTCAATTTTGGTCAAGCTGCGACT 2742
Db 2698 TTGCGAAGAGGCGCAGCAGCCGCTTAAAGAGACTCAATTTTGGTCAAGCTGCGACT 2757
OY 2743 CAGAGTCAAGTCCCGGACCCCAACCTCTCGAGAACTTCAGCAACCCCGCTGTGTGG 2802
Db 2758 CAGAGTCAAGTCCCGGACCCCAACCTCTCGAGAACTTCAGCAACCCCGCTGTGTGG 2817
OY 2803 GACTTACTTAACATGCTTCAAGCGGCTGAGGCGCAACATGAGAGCAATTAAGAGGCGCG 2862
Db 2818 GACTTACTTAACATGCTTCAAGCGGCTGAGGCGCAACATGAGAGCAATTAAGAGGCGCG 2877
OY 2863 ACGGAGTGGGTAAATGCTCTAGAGAAATTTGCAATTTGCAATCTCAATGCTGGGCGAGAG 2922
Db 2878 ACGGAGTGGGTAAATGCTCTAGAGAAATTTGCAATTTGCAATCTCAATGCTGGGCGAGAG 2937
OY 2923 TCATCACCAAGCAACCGCAACATGAGGCTTGGCCACTATTAACCACTCTACAGAGC 2982
Db 2938 TCATCACCAAGCAACCGCAACATGAGGCTTGGCCACTATTAACCACTCTACAGAGC 2997
OY 2983 AAATCTCAAGTCTTCAACGCGGCGCAAGCAACCACTCTCGGCTACAGAGCC 3042
Db 2998 AAATCTCAAGTCTTCAACGCGGCGCAAGCAACCACTCTCGGCTACAGAGCC 3057
OY 3043 CTTGGGGGTATTTGATTTTCAACAGATTTCCACTGCAATTTCTGACCAAGTACGAGCAGC 3102
Db 3058 CTTGGGGGTATTTGATTTTCAACAGATTTCCACTGCAATTTCTGACCAAGTACGAGCAGC 3117
OY 3103 GACTCATCAACCAATTTGGGAGTTCCGCGCCAAAGAGACTCAACCTTCAAGCTCTTCAAC 3162
Db 3118 GACTCATCAACCAATTTGGGAGTTCCGCGCCAAAGAGACTCAACCTTCAAGCTCTTCAAC 3177
OY 3163 TCCAGTCAAGAGAGTCAACAGATGATGAGCGTCAAGCACTGCGTAATTAACCTTAACGA 3222
Db 3178 TCCAGTCAAGAGAGTCAACAGATGATGAGCGTCAAGCACTGCGTAATTAACCTTAACGA 3237
OY 3223 GCAAGTTCAGATTTTGTGCGACTCGGAGTCAAGATTTCCGCTACGCTCTGCGCTTGGCG 3282
Db 3238 GCAAGTTCAGATTTTGTGCGACTCGGAGTCAAGATTTCCGCTACGCTCTGCGCTTGGCG 3297
OY 3283 ACGAGGCGCTCTCCCTCCGTTCCCGGCGGAGCTGTTCAATGATTTCCGAGTAAAGCTAAC 3342

OY	343	GATTTAAGGTCCCCAGCCGACCTTTGAACGAGCACTCTGCGCGGCAATTTCTGACACGCTTTGTGAA	402
Db	358	GATCAAGGTGTGCGAGCCGACTGTGACGAGACACTGTGCGGGCAATTTCTGACTGTGTGTGAG	417
OY	403	CTGGGTGGCCGAGAAAGAAATGGGAGTTTGCCTGCGCAGATTTCTGACATGGATCTGAAATCTGAT	462
Db	418	CTGGGTGGCCGAGAAAGAAATGGAGACTGCCCCCGGATTTCTACATGGATCTGAAATCTGAT	477
OY	463	TGAGCAGGCAACCCCTGACCGTGTGCGAGAACCTGACAGCGACACTTCTGTGATCCACTGGCG	522
Db	478	TGAGCAGGCAACCCCTGACCGTGTGCGAGAACCTGACAGCGACACTTCTGTGATCCAATGGCG	537
OY	523	CCGGGTGAGTAAAGGCCCGGAGAGCCCTCTTCTTTGTTGATTTGAGAAAGGCGAGTCTTA	582
Db	538	CCGGGTGAGTAAAGGCCCGGAGAGCCCTCTTCTTTGTTGATTTGAGAAAGGCGAGTCTTA	597
OY	583	CTTCCACCTCCATATTTCTGTGTGAGACCAAGGGGGTCAAACTCAATGGGTGCTGGGCGGCTT	642
Db	598	CTTCCACCTCCATATTTCTGTGTGAGACCAAGGGGGTCAAACTCAATGGGTGCTGGGCGGCTT	657
OY	643	CCTGAGTCAATTAAGCCGACAAGCTGTGTGACACATCTTACCGCGGAGATCGAGCCGACCT	702
Db	658	CCTGAGTCAATTAAGGAGCAAGCTGTGTGACACATCTTACCGCGGAGATCGAGCCGACCT	717
OY	703	GCCCAACTGTGTTCCGCGTGTGCCAAGACGCGTAAATGGCCGCGAGGGGGGAAACAAGTGT	762
Db	718	GCCCAACTGTGTTCCGCGTGTGCCAAGACGCGTAAATGGCCGCGAGGGGGGAAACAAGTGT	777
OY	763	GGAAGAGTGTAACTATCCGCAACTACCTCTGTGCGCCAAAGACTGAGCCGAGCTGTGAGTGGC	822
Db	778	GGAAGAGTGTAACTATCCGCAACTACCTCTGTGCGCCAAAGACTGAGCTGTGAGTGGC	837
OY	823	GTGCACTAACTGAGAGGATATTAAGCGCGTGTTTAACTGTGCGAGCCGACCAACGACT	882
Db	838	GTGCACTAACTGAGAGGATATTAAGCGCGTGTTTAACTGTGCGAGCCGACCAACGACT	897
OY	883	CGTGGCGCACGACTGTGACCCACGTGACGCAACAACGAGAGCAAAAGAGAAATCTGAA	942
Db	898	CGTGGCGCACGACTGTGACCCACGTGACGCAACAACGAGAGCAAAAGAGAAATCTGAA	957
OY	943	CCCCAATTTCTACCGGCGCTGTCAATCCGGTCAAAAACCTCCGACGCTTCAATGAGACTGGT	1002
Db	958	CCCCAATTTCTACCGGCGCTGTCAATCCGGTCAAAAACCTCCGCGCTTCAATGAGACTGGT	1017
OY	1003	CGGGTGGCTGTGTGAGACCGGGGCACTCACTCCGAGAAAGATGTGATCCAGAGAGCAAGGC	1062
Db	1018	CGGGTGGCTGTGTGAGACCGGGGCACTCACTCCGAGAAAGATGTGATCCAGAGAGCAAGGC	1077
OY	1063	CTCGTACATCTTCTTCAACGCGCGCTTCAACTGTGCGGTCCAGATCAAGGCGCGTCTGA	1122
Db	1078	CTCGTACATCTTCTTCAACGCGCGCTTCAACTGTGCGGTCCAGATCAAGGCGCGTCTGA	1137
OY	1123	CAATGCCCGGCAAGATCATTGGCGCTTCAACCAATCCGCGCCGACATCTGTGATGAGCCCGC	1182
Db	1138	CAATGCCCGGCAAGATCATGTGGCGCTTCAACCAATCCGCGCCGACATCTGTGATGAGCCCGC	1197
OY	1183	TCCGCGCGGCGCATTTAAACCAACGCGATTTACCGCATCTGTGAGCTGAAACGCGTACGA	1242
Db	1198	TCCGCGCGGCGCATTTAAACCAACGCGATCTTACCGCATCTGTGAGCTGAAACGCGTACGA	1257
OY	1243	CCCTGCTTACGCGCGGCTCCGTCTTCTGTGCGTGGGCGCAGAAAAGTTTCGAAAAACGCA	1302
Db	1258	ACCTGCTTACGCGCGGCTCCGTCTTCTGTGCGTGGGCGCAGAAAAGTTTCGAAAAACGCA	1317
OY	1303	CACCATCTGTGCTGTTTGGGCGCGGCAACAACGCGGCAAGACCAACATCGCGAAAGCATGTGC	1362
Db	1318	CACCATCTGTGCTGTTTGGGCGCGGCAACAACGCGGCAAGACCAACATCGCGAAAGCATGTGC	1377
OY	1363	CCAGGCGGTGCTTCTTACGCGGTGGGTCAACCTGAGCAATATGAACTTTCCCTTCAACGA	1422
Db	1378	CCAGGCGGTGCTTCTTACGCGGTGGGTCAACCTGAGCAATATGAACTTTCCCTTCAACGA	1437
OY	1423	TTGCTCTGCAACAAGATGTGATCTGTGTGGAGAGGAGCAAGATGACGCGCAAGATCTGTGA	1482

Db	1438	TTGCTGCAACAAGTGGTGAATCTGTGTGGAGAGAGGCAAGATGACGGCCAAAGGTCGTGGA	1497
Oy	1483	GTCCGCCAAGGCCATTTCTCGCGCGGCAACAAGTGTCGGTGAACCAAAAGTGCAAGTCGC	1542
Db	1498	GTCCGCCAAGGCCATTTCTCGCGCGGCAACAAGTGTCGGTGAACCAAAAGTGCAAGTCGC	1557
Oy	1543	CGCCCAAGATGATCCACCCCGGTGATGTCGACCTTCCAAACAACATGTGCCCGGTGAT	1602
Db	1558	CGCCCAAGATGATCCACCCCGGTGATGTCGACCTTCCAAACAACATGTGCCCGGTGAT	1617
Oy	1603	TGACGGGAACAAGCAACAATTCCAGACACAGACGCGTTGCAGAGGACCGAATGTTCAATT	1662
Db	1618	TGACGGGAACAAGCAACAATTCCAGACACAGACGCGTTGCAGAGGACCGAATGTTCAATT	1677
Oy	1663	TGAACCTACCCGCGCGTCTGGAGCATGACTTTGGCAAGTGACAAAGCAGGAAAGTCAAGA	1722
Db	1678	TGAACCTACCCGCGCGTCTGGAGCATGACTTTGGCAAGTGACAAAGCAGGAAAGTCAAGA	1737
Oy	1723	GTTCTTCCTCGCTGGGCGCAGATCACTGTACCGAGTGTCGCGCATGATGTTCTACGTCAAAA	1782
Db	1738	GTTCTTCCTCGCTGGGCGCAGATCACTGTACCGAGTGTCGCGCATGATGTTCTACGTCAAAA	1797
Oy	1783	GGGTGGAGCCAAACAAGACCCCGCGCGCATGACGCGGATATPAAAAGGAGGCCAAAGCGGGC	1842
Db	1798	GGGTGGAGCCAAACAAGACCCCGCGCGCATGACGCGGATATPAAAAGGAGGCCAAAGCGGGC	1857
Oy	1843	CTGCCCCCTCAGTCCGCGATCCATGACGTGACAGCGCGGAAGAGCTCCGGTGAACCTTTGC	1902
Db	1858	CTGCCCCCTCAGTCCGCGATCCATGACGTGACAGCGCGGAAGAGCTCCGGTGAACCTTTGC	1917
Oy	1903	CGACAGGTACCAAAACAATGTTCTCGTCAACGCGGGCATGCTTCAGATGCTGTTCCCTG	1962
Db	1918	CGACAGGTACCAAAACAATGTTCTCGTCAACGCGGGCATGCTTCAGATGCTGTTCCCTG	1977
Oy	1963	CAAAACAATCGCAGAGATGAAATCGAATTTCAACATTTGCTTCAACGAGGACCAAGA	2022
Db	1978	CAAAACAATCGCAGAGATGAAATCGAATTTCAACATTTGCTTCAACGAGGACCAAGA	2037
Oy	2023	CTGTTCAAGAAATGTTTCCCGCGCGTGCAGAAATCTCAACCGGTGCTCGAAAGAGAGCGTA	2082
Db	2038	CTGTTCAAGAGTCTTCCCGCGCGTGCAGAAATCTCAACCGGTGCTCGAAAGAGAGCGTA	2097
Oy	2083	TCGGAAAATCTGTGCCAATTCATCATCTGTGGGGCGGGCTCCCGAGATTCCTGTCTCGC	2142
Db	2098	TCGGAAAATCTGTGCCAATTCATCATCTGTGGGGCGGGCTCCCGAGATTCCTGTCTCGC	2157
Oy	2143	CTGCGATCTGGTCAACGTGATCTTGGATGACTGTGTTCTTGAGCAATAAATGACTTTAAAC	2202
Db	2158	CTGCGATCTGGTCAACGTGATCTTGGATGACTGTGTTCTTGAGCAATAAATGACTTTAAAC	2217
Oy	2203	CAGGTATGGCTGCCGATGTTATTTCCAGATTGGCTCGAGAGCAACCTCTCTGAGGGCA	2262
Db	2218	CAGGTATGGCTGCCGATGTTATTTCCAGATTGGCTCGAGAGCAACCTCTCTGAGGGCA	2277
Oy	2263	TTTCGGCAGTGTGGGACTTGAAACCTTGAAGCCCGAAACCCAAAGCCAAACGCAAAAGC	2322
Db	2278	TTTCGGCAGTGTGGGACTTGAAACCTTGAAGCCCGAAAGCCCAAGCCAAACGCAAAAGC	2337
Oy	2323	AGACGACGCGCGGGGCTGTGTGCTTCTTGCTTCAAGTACCTTGGACCTTTCAAGGAC	2382
Db	2338	AGACGACGCGCGGGGCTGTGTGCTTCTTGCTTCAAGTACCTTGGACCTTTCAAGGAC	2397
Oy	2383	TCGACAAGGGGGAGCCCGTCAACGCGGGGAGTGAAGGGGCGCTGAGACGACGCAAGGCT	2442
Db	2398	TCGACAAGGGGGAGCCCGTCAACGCGGGGAGTGAAGGGGCGCTGAGAGCGACGCAAGGCT	2457
Oy	2443	ACGACACGACACTCAAAAGCGGTGACATCCGTACTGCGGTATATACACGCGCAGCGCG	2502
Db	2458	ACGACACGACACTCAAAAGCGGTGACATCCGTACTGCGGTATATACACGCGCAGCGCG	2517
Oy	2503	AGTTTCAGAGCGTCTGCAGAGATACGTTTTCGGGGCAACCTTGGGCGAGCGAGTCT	2562

Dh 2518 AGTTTCAGAGGCTCTGCAGAGATACGTCCTTTTGGGGGCAACCTCGGGGCGAGACGCT 2577
Qy 2563 TCCAGGCCAAGAAAGGGTTCTCGAACCTTTTGGTCTGTTGAGGAAGGTGCTAAGACGG 2622
Dh 2578 TCCAGGCCAAGAAAGGGTTCTCGAACCTCTCGGCTGTGGTGAAGAAAGCGCTAAGACGG 2637
Qy 2623 CTCTGGAAGAAAGAGTCCGGTAGAGCAGTCGCAAGAGGCAAGACTCTCTCGGGCA 2682
Dh 2638 CTCTGGAAGAAAGAGTCCGGTAGAGCAGTCGCAAGAGGCAAGACTCTCTCGGGCA 2697
Qy 2683 TTGGCAAGACAGGCCAGAGCCCGCTAAAGAGCTCAATTTTGGTGAAGCTGAGACT 2742
Dh 2698 TCGGCAAGACAGGCCAGAGCCCGCTAAAGAGCTCAATTTTGGTGAAGCTGAGACT 2757
Qy 2743 CAGAGTCAGTCCCGACCCCAACACTCTCGAGAACTCTCGACAAACCCCGCTGTTGG 2802
Dh 2758 CAGAGTCAGTCCCGACCCCAACACTCTCGAGAACTCTCGACAAACCCCGCTGTTGG 2817
Qy 2803 GACCTACTACATAGGCTTCAGGCGGTGGCGCACCAATGGCAGACAAATAAGAGGCGCG 2862
Dh 2818 GACCTACTACATAGGCTTCAGGCGGTGGCGCACCAATGGCAGACAAATAAGAGGCGCG 2877
Qy 2863 ACGAGTGGGTATGCTCAGAGAAATTGGCAATTGGCAATTCATGCTGGGCGACAG 2922
Dh 2878 ACGAGTGGGTATGCTCAGAGAAATTGGCAATTGGCAATTCATGCTGGGCGACAG 2937
Qy 2923 TCATCAACACAGCACCCGAAATGGCTTGGCCACTTATACCAACCTCTTACAGC 2982
Dh 2938 TCATCAACACAGCACCCGAACTGGGGCTTGGCCACTTACATTAACCACTCTTACAGC 2997
Qy 2983 AATCTCCAGTCTTCAACGGGGGCGCAGCAAGCAACCACTACTTGGGCTTACAGCACCC 3042
Dh 2998 AATCTCCAGTCTTCAACGGGGGCGCAGCAAGCAACCACTACTTGGGCTTACAGCACCC 3057
Qy 3043 CTTGGGGGTATTTGATTTCACAGATTCATGCTCATTTCTACACAGGTGACCTGGCAGC 3102
Dh 3058 CTTGGGGGTATTTGATTTCACAGATTCATGCTCATTTCTACACAGGTGACCTGGCAGC 3117
Qy 3103 GACTCATCAACAAATTTGGGGATTCGGGCCCAAGAGCTCACTTCAAGCTTTCAACA 3162
Dh 3118 GACTCATCAACAAATTTGGGGATTCGGGCCCAAGAGCTCACTTCAAGCTTTCAACA 3177
Qy 3163 TCCAAAGTCAGAGGCTCAGACGAATGATGGGTGACAGACATGCTAATAACCTTACCA 3222
Dh 3178 TCCAAAGTCAGAGGCTCAGACGAATGATGGGTGACAGACATGCTAATAACCTTACCA 3237
Qy 3223 GCACGGTTCAAGTCTTGTGAGACTCGAGTACCAAGTCCGTAAGTCTCTCGGCTCTGGC 3282
Dh 3238 GCACGGTTCAAGTCTTGTGAGACTCGAGTACCAAGTCCGTAAGTCTCTCGGCTCTGGC 3297
Qy 3283 ACCAGGGCTGCTCTCTCGGTTCCGGGCGAACGTGTCATGATTTCCGCAATAACGCTACCC 3357
Dh 3298 ACCAGGGCTGCTCTCTCGGTTCCGGGCGAACGTGTCATGATTTCCGCAATAACGCTACCC 3357
Qy 3343 TAAAGCTCAACAAATGGGAGCGAGGAGTGGAGCGCTACCTTTTAACTGCGTGAATTT 3402
Dh 3358 TGAAGCTCAACAAATGGGAGCGAGGAGTGGAGCGCTACCTTTTAACTGCGTGAATTT 3417
Qy 3403 TCCCATCGAGATCTGAGAACGGGCAATTAATTTTACCTTACAGTCAACCTTTCGAGAGC 3462
Dh 3418 TCCCATCGAGATCTGAGAACGGGCAATTAATTTTACCTTACAGTCAACCTTTCGAGAGC 3477
Qy 3463 TGCTTTTCCAGAGAGTACGCGGCAACGCGCAGAGCTTGGACCGGTGATGAATCTCTCA 3522
Dh 3478 TGCTTTTCCAGAGAGTACGCGGCAACGCGCAGAGCTTGGACCGGTGATGAATCTCTCA 3537
Qy 3523 TCGACCAATACCTGATTAATCTGAAACAGAACTCAAAATCACTCGGAAAGTCCCAAAACA 3582
Dh 3538 TCGACCAATACCTGATTAATCTGAAACAGAACTCAAAATCACTCGGAAAGTCCCAAAACA 3597
Qy 3583 AGGACTGTGTTTAAAGCGGTGGTCTCCAGCTGGCAGTGTCTTCAAGCCAAAAACTGGC 3642
Dh 3598 AGGACTGTGTTTAAAGCGGTGGTCTCCAGCTGGCAGTGTCTTCAAGCCAAAAACTGGC 3657

Qy 3643 TACCTGACCCCTGTTACCGGAGAGCGCGCTTCTAAACAAACAAAGACAAACAACA 3702
Dh 3658 TACCTGACCCCTGTTATTCGAGAGCGCGTTTCTAAACAAACAAAGACAAACAACA 3717
Qy 3703 GCAACTTATCTGAGACTGCTCTTCAAAATTAACCTTAAATGGGCGTGAATCTAATCA 3762
Dh 3718 GCAATTTTACTGAGACTGCTCTTCAAAATTAACCTTAAATGGGCGTGAATCTAATCA 3777
Qy 3763 ACCCTGACCTGCTATGAGCTCTCAACAAGACGACAAAGACAGTCTTTTCCATGAGCG 3822
Dh 3778 ACCCTGACCTGCTATGAGCTCTCAACAAGACGACAAAGACAGTCTTTTCCATGAGCG 3837
Qy 3823 GTGTCAATGATTTTGGAAAGAGAGCGCGGAGCTTCAACACTGCAATTTGACATGCA 3882
Dh 3838 GTGTCAATGATTTTGGAAAGAGAGCGCGGAGCTTCAACACTGCAATTTGACATGCA 3897
Qy 3883 TGATCAACAGAGAGAGAAATCAAAAGCACTAACCCCGTGGCCACGAAAGATTTGGGA 3942
Dh 3898 TGATCAACAGAGAGAGAAATTAAGCCACTAACCTGTGGCCACGAAAGATTTGGGA 3957
Qy 3943 CTGTGGAGTCAATCTCCAGAGCAGACAGACAGACCTTGGCAGCGAGATGTGATGTTA 4002
Dh 3958 CCGTGGAGTCAATTTTCCAGAGCAGACAGACAGACCTTGGCAGCGAGATGTGATGTTA 4017
Qy 4003 TGGAGACCTTACCTGGAATGTGTGGCAAGACAGAGAGTATCTGAGAGGTCTTATT 4062
Dh 4018 TGGAGACCTTACCTGGAATGTGTGGCAAGAGTATGAGAGTATCTGAGAGGTCTTATT 4077
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Dh 4078 GGGCCAAATTCCTCACAAGGATGGAACATTTCAACCCGTCTCTCATGAGGGCGCTTGG 4137
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Dh 4138 GACTTAAAGACCCGCTCTCTCAGATCTCATCAAAAACAGCCTGTTCTTGGATCTTC 4197
Qy 4183 CGGAGAGTTTGGGCTTCAAAAGTTTGGCTTCAATTCATCCCAATTAATTTCCACAGAG 4242
Dh 4198 CGGAGAGTTTGGGCTTCAAAAGTTTGGCTTCAATTCATCCCAATTAATTTCCACAGAG 4257
Qy 4243 TGAAGCTGAGATTAATGAGAGTGGAGCTGAGAAAGAAACAGCAACGCTGAAATCCGAG 4302
Dh 4258 TGAAGCTGAGATTAATGAGAGTGGAGCTGAGAAAGAAACAGCAACGCTGAAATCCGAG 4317
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LOCUS
DEFINITION Sequence 6 from Patent EP1310571.
ACCESSION AX753251
VERSION AX753251.1 GI:32166108
KEYWORDS
SOURCE Adeno-associated virus - 1
ORGANISM Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
REFERENCE 1
AUTHORS Geo, G., Wilson, J.M. and Alvira, M.
TITLE A method of detecting and/or identifying adeno-associated virus (ADV) sequences and isolating novel sequences identified thereby
JOURNAL Patent: EP 1310571-A 6-14-MAY-2003,
The Trustees of The University of Pennsylvania (US)
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Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;
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ACCESSION	AF063497		
VERSION	AF063497.1	GI:4689096	
KEYWORDS	Adeno-associated virus - 1		
SOURCE	Adeno-associated virus - 1		
ORGANISM	Adeno-associated virus - 1		
REFERENCE	Adeno-associated virus - 1		
AUTHORS	Xiao,W., Chimumle,N., Berta,S.C., McCullough,B., Gao,G. and Wilson,J.M.		
TITLE	Gene therapy vectors based on adeno-associated virus type 1		
JOURNAL	J Virol. 73 (5), 3994-4003 (1999)		
PIRMBD	2 (bases 1 to 4718)		
REFERENCE	Xiao,W. and Wilson,J.M.		
AUTHORS	Xiao,W. and Wilson,J.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601		

FEATURES		Spruce Street, Philadelphia, PA 19104, USA	
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Db 718 GCCCACTGTTTCGGGTGACCAAGACGCGTAATGGCGCGGAGGGGAGAACTAGTGT 777
Qy 763 GGAAGAGTCTACATTTCCCACTACCTCTGCGCCAGACTGAGCCCCGAGCTGAGTGGG 822
Db 778 GGAAGAGTCTACATTTCCCACTACCTCTGCGCCAGACTGAGCCCCGAGCTGAGTGGG 837
Qy 823 GTGACTTAACATGAGAGAGATATATAGGCGGTGTTTAACTGAGCGGAGCAAACTGCT 882
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Qy 1063 CTGCTACATCTCTTCAACGCGCGCTCCAACTCCGCGATCCAGATCAAGGCGCTTGA 1122
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LOCUS CO972062 Sequence 7 from Patent WO2004108922.
DEFINITION CO972062
ACCESSION CO972062.1 GI:57163375
VERSION CO972062.1
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SOURCE Adeno-associated virus
ORGANISM Adeno-associated virus
Virus; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
unclassified Dependovirus.
REFERENCE
1 Rader,D.J. and Wilson,J.M.
AUTHORS Methods and compositions for lowering total cholesterol levels and
TITLE Treatment of heart disease
JOURNML Patent: WO 2004108922-A 7 16-DEC-2004;
The Trustees of The University of Pennsylvania (US)
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SOURCE
ORGANISM
unclassified
unclassified
unclassified sequences.

REFERENCE 1
AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenbergh, L.H.
TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses therefor
JOURNAL Patent: WO 2005033321-A 180 14-APR-2005;
The Trustees of the University of Pennsylvania (US)
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ACCESSION AX753246
VERSION AX753246.1 GI:32166105
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ORGANISM
Adeno-associated virus - 7
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
unclassified Dependovirus.
REFERENCE
1 Gao, G., Wilson, J.M. and Alvira, M.
A method of detecting and/or identifying adeno-associated virus
(AAV) sequences and isolating novel sequences identified thereby
Patent: EP 1310571-A.1 14-MAY-2003;
The Trustees of The University of Pennsylvania (US)
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Db 181 GTAATGACGTGATAGGG---GAGTGTCTGTATTAGCTGACGTGAGTGTTCG 237
Qy 224 ACATTTTGGGACACCATGTGTGTCAGCTGGGTATTGAACCCGAGTGGACAGAGGTC 283
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Qy 284 TCCATTTTGAAGCGGAGGATTGGAACCGGACAGCCATGCGGGTTTGAAGATTGTG 343
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Qy 344 ATTAAGTCCCGACGACCTTTGACGAGCATCTGCGGCATTTTGAACGCTTTGTGAAC 403
Db 358 ATCAAGGTGCGAGGACCTGGAAGACCTGCGGGCATTTTGAAGCTTTGTGAAC 417
Qy 404 TGGGTGCGGAGGAAGGATGGGAGTGGCCGCAATTTGACATGATCTGAATCTGATT 463
Db 418 TGGGTGCGGAGGAAGGATGGGAGTGGCCGCAATTTGACATGATCTGAATCTGATT 477
Qy 464 GAGCAGGACCCCTGACCGTGGCCGAGAGCTGACGAGCGACTTCCTGTGCACTGGGCG 523
Db 478 GAGCAGGACCCCTGACCGTGGCCGAGAGCTGACGAGCGACTTCCTGTGCAATGGGCG 537
Qy 524 CGCGTGAATAGGCGCCGAGGCGCTCTTCTTTGTTCAGTTGAGAGGCGAGTCTTAC 583
Db 538 CGCGTGAATAGGCGCCGAGGCGCTCTTCTTTGTTCAGTTGAGAGGCGAGTCTTAC 597
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Db 718 CCGAATGTGTGCGGTGACCAAGCGGTATGGCGCGGAGGGGGGACAAAGGTGTG 777
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Qy 1064 TCGTACATCTCTTCAACCGCGCTCAACTGCGGTCCAGATCAAGCGCGCTGTGAC 1123
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Qy 2324 GAGAGAGCGCGGGGTGTGGTCTTCTGAGTCAAGTACTGAGACCTTCAACGAGACT 2383
Db 2338 GAGAGAGCGCGGGGTGTGGTCTTCTGAGTCAAGTACTGAGACCTTCAACGAGACT 2397

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QY 4178 TCTCCGGGAGAGTTTGGGCTCAAAAGTTTGTCTCAATTCATCAACCAAGTATTCACAG 4237
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Db 4195 TCTCCGGGAGAGTTTGGGCTCAAAAGTTTGTCTCAATTCATCAACCAAGTATTCACAG 4254
QY 4238 ACAAGTAGCGTGAAGTGAATGAGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCC 4297
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QY 4358 CAATGACTTATTAACAGAGCTGCGCCATTTGGGACCGGTTACCTGACCGGCTCCGTA 4417
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QY 4418 ATTGTGTATTAATCAATTAACCGGTTAATCGTGTAGTTGAACCTTGTGCTCATGTCT 4477
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QY 4478 TATTAATCTTAATGAGTCAATGAGCAGGTTAACAATTAATGCTTAATGCGGCTTCG 4537
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Db 4495 TCTTAATCTTAATGAGTCAATGAGCAGGTTAACAATTAATGCTTAATGCGGCTTCG 4553
QY 4538 CGA-----ATACCCCTAGTATGAGTGAAGTGGCCACTCCCTATAT 4575
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[illegible]

Query Match	78.5%	Score 3678.4	DB 10	Length 4721
Best Local Similarity	87.5%	Pred. No. 0		
Matches 4135	Conservative 0	Mismatches 541	Indels 52	Gaps 8
QY	1	TTGGCAATCCCTCTCTCCGCGCTCGCTCGCTCACTGAGCGCCGCGCGCAACAAAGGTCCGC	60	
Db	1	TTGGCACTCCCTCTATCGCGCTCGCTCGCTCGCTCGCTGGGGGCTGGGACCAAGGTCCGC	60	
QY	61	CGAGCCCGGGCTTTGCGCCGGCGGCTCAGTGAAGCGAGCGCGAGAGAGAGAGT	120	
Db	61	AGACGCGAGAGACTGCTCTCTCCGGCCCAACGAGCGAGCGCGATAGAGGAGT	120	
QY	121	GCCAACTCCATCACTAGGGGTTCTCGAGG-----GGTGAATCTGTAAC	164	
Db	121	GCCAACTCACTACAGGGGTACCGCGAAGCGGCTCCACGCTGCGCGTACGCGCTAAC	180	
QY	165	GTGAATTACGTATAGGGTTTAGGAGGTCCTGTATTAAGTCACTGTAGTG-TTTTGCG	223	
Db	181	GTAAATACGTCATATAGGG--GAGTGCTCTGTATTAAGTCACTGTAGTCTTTTTCG	237	
QY	224	ACATTTTTCGACACCATGTGTCACGCTGGGTATTTAAGCCCGATGACGACGAGGTC	283	
Db	238	ACATTTTTCGACACACAGTGCCATTTAGGTATATATAGGCGATGACGAGCGAGATC	297	
QY	284	TCCATTTTGAACGGGAGGTTTGAACGCGCACCGCCATGCGGGGTTTATGAGATTGTG	343	
Db	298	TCCATTTTGAACCGCGAATTTTGAACGACAGCAGCAGCCAGTTCGCGGTTTCTACAGATCGTG	357	
QY	344	ATTAAAGTCCCAAGGACCTTGAGAGAGATGCGCCGGCATTTCTGACAGCTTGTGTAAAC	403	
Db	358	ATCAAGGTCCGAGGACCTTGAGAGACCTTGCCGGCATTTCTGACTCGTTGTGTAAAC	417	
QY	404	TGGGTGCGGAGAAAGAAATGGAGATTGCGGCAGATTCTGACATGATCTGAATCTGAAT	463	
Db	418	TGGGTGCGGAGAAAGAAATGGAGATTGCGGCAGATTCTGACATGATCTGAATCTGAATC	477	
QY	464	GAGCAGGCAACCCCTGACCTGTGGCGGAGAAAGCTGACAGCGCCGACTTCTGTGTCACTGGGCG	523	
Db	478	GAGCAGGCAACCCCTGACCTGTGGCGGAGAAAGCTGACAGCGCCGACTTCTGTGTCAAGTGGGCGC	537	
QY	524	CGCGGATTAAGGCCCGGAGGCGCTTCTTCTTGTTCAGTTTGAGAAAGGCGAGTCTAC	583	
Db	538	CGCGGATTAAGGCCCGGAGGCGCTTCTTCTTGTTCAGTTTCAGAAAGGCGAGGCTAC	597	
QY	584	TTCCACCTCCATATTCTGTGTGAGACCAACGCGGGGCTCAATCCATGTGCTGGGCGCTTC	643	
Db	598	TTCCACCTCCACGTTCTGTGTGAGACCAACGCGGGGCTCAATGTGTGCTGAGCGGCTTC	657	
QY	644	CTGAGTCAAGTTAAGGACAAAGCTGTGTGAGACCACTTACCGCGGAGTGAACCCGACCTG	703	
Db	658	CTGAGTCAAGTTAAGGACAAAGCTGTGTGAGACCACTTACCGCGGGGTGAGACCCGACCTG	717	
QY	704	CCCAACTGATTGCGCGTGACCAAGACGGTATGGGCGCGGAGGGGGGAAACAAGTGTGTG	763	
Db	718	CCCAACTGATTGCGCGTGACCAAGACGGTATGGGCGCGGAGGGGGGAAACAAGTGTGTG	777	
QY	764	GACGAGTCTACATCCCAACTACTCTCTGCCCCAAGACTAGCCCGAGCTGATGGGCG	823	
Db	778	GACGAGTCTACATCCCAACTACTCTCTGCCCCAAGACCAAGCCCGAGCTGATGGGCG	837	
QY	824	TGGAATTAATGAGGAGATATATAGCGCGGTTTAAACTGTGGCGGACCGCAACGAGGCTC	883	
Db	838	TGGAATTAATGAGGAGATATATAGCGCGGTTTGAACCTGGCGGACCGCAACGAGGCTC	897	

QY	884	GTGGCGACGACCTTGACCCACGTGACGCCAGACCAGAGCGAACAAGAGAAATCTGAAC	943
Db	898	GTGGCGCGACGACCTTGACCCACGTGACGCCAGAGCGCAGAGCGAAGAACAGAAATCTGAAC	957
QY	944	CCCAATTTCTGACGGCGCTCTGTACATCCGGTCAAAAAACCTCCGCAACGCTAATATGACCTGGTC	1003
Db	958	CCCAATTTCTGACGGCGCTCTGTACATCCGGTCAAAAAACCTTCGGCGCTCAATGACAGCTGGTC	1017
QY	1004	GGGTGGCTGTGGTGAACCGGGGACATCACTCCGAGAAAGAGTGGATTCAGAGAGAACCGAGCC	1063
Db	1018	GGGTGGCTGTGGTGAACCGGGGACATCACTCCGAGAAAGAGTGGATTCAGAGAGAACCGAGCC	1077
QY	1064	TCGTACATCTCTTCAACGCGCGCTTCAACTTCGCGTCCAGATCAAGCGCTCTGGAC	1123
Db	1078	TCGTACATCTCTTCAACGCGCGCTTCAACTTCGCGTCCAGATCAAGCGCGCTCTGGAC	1137
QY	1124	AATGCGGGCAAGATCATATGGCGCTGAACCAATTCGCGCGCCGACTACCTTGTAAGCCCGCT	1183
Db	1138	AATGCGGGCAAGATCATATGGCGCTGAACCAATTCGCGCGCCGACTACCTTGTAAGCCCGCTCG	1197
QY	1184	CGCGCCGCGGACATTTAAACCAACCGGATTTTACCGCATCTTGAGACTGAACGGCTACAGAC	1243
Db	1198	CTGCCCCGGGACATTTAAACCAACCGCATCTTACCGCATCTTGAGACTGAACGGGTACAT	1257
QY	1244	CCTGCTTACGCGCGCTCCGCTTTTCTCGGCTGGGCCCAAAAAAGTTTCGAAAAACGCAAC	1303
Db	1258	CCTGCTTACGCGCGCTCCGCTTTTCTCGGCTGGGCCCAAAAAAGTTTCGGAAGCGCAAC	1317
QY	1304	ACCATCTGGCTGTTTGGGCGGGCCACACACGGGCAACCAACATTCGGGAAGCCATCGCC	1363
Db	1318	ACCATCTGGCTGTTTGGGCGGGCCACACACGGGCAACCAACATTCGCGGAAGCCATCCCC	1377
QY	1364	CACGCGGAGCCCTTCTAGGGCTGGGCTCAACTGGACCAATTTGAATCTTCCCTTCAACGAT	1423
Db	1378	CACGCGGAGCCCTTCTAGGGCTGGGCTCAACTGGACCAATTTGAATCTTCCCTTCAACGAT	1437
QY	1424	TGCGTGCACAAGATGTGTATCTGTGTGGAGAGAGGCAAGATGACGGCCAAAGTCTGTGAG	1483
Db	1438	TGCGTGCACAAGATGTGTATCTGTGTGGAGAGAGGCAAGATGACGGCCAAAGTGTGTGAG	1497
QY	1484	TCGCGCAAGGCCATTTCTGGCGGGACGAAAGTGGCCGTGGACCAAAAGTGCAGATCTGCC	1543
Db	1498	TCGCGCAAGGCCATTTCTGGCGGGACGAAAGTGGCCGTGGACCAAAAGTGCAGATCTGCC	1557
QY	1544	GCCGCAATCGATCCCAACCCCGGTGATGTCACCTTCAACCAACCAATGGGCGGTGATT	1603
Db	1558	GCCGCAATCGATCCCAACCCCGGTGATGTCACCTTCAACCAACCAATGGGCGGTGATT	1617
QY	1604	GACGGGAACAGACCACTTCAGAGACGACGACGCGTTGACAGAACCGGATGTTCAAAATTT	1663
Db	1618	GACGGGAACAGACCACTTCAGAGACGACGACGCGTTGACAGAACCGGATGTTCAAAATTT	1677
QY	1664	GAAGTCAACCCGCGCTGTGAGAGCATGACTTTGGCAAGGTGACAAAGACGAGAAATCTGAAG	1723
Db	1678	GAAGTCAACCCGCGCTGTGAGAGCATGACTTTGGCAAGGTGACGAAACGAGAAATCTGAAG	1737
QY	1724	TTTCTTCCGCTGGGCGGACGAGATTCAGGTGACCGAGGTGGGCGAATGATTTCTAGGTGAAAG	1783
Db	1738	TTTCTTCCGCTGGGCGGACGAGATTCAGGTGACCGAGGTGGGCGAATGATTTCTAGGTGAAAG	1797
QY	1784	GGTGAGAGCAACACAGACCGCGCCCCGATGACGGGTGAATTAAGAGAGACCCCAAGCGGCGC	1843
Db	1798	GGTGAGAGCAACACAGACCGCGCCCCGATGACGGGTGAATTAAGAGAGACCCCAAGCGGCGC	1857
QY	1844	TGCCCCCTCAATCGCGGATTCATGACGCTGACGCGGGAAGAGCTTCGAGTGAATTTTCC	1903
Db	1858	TGCCCCCTCAATCGCGGATTCATGACGCTGACGCGGGAAGAGCTTCGAGTGAATTTTCC	1917
QY	1904	GACAGGTTCACAAACAAATGTTTCTGTGACCGGGGACATGCTTCAATGCTGTTTCCCGC	1963
Db	1918	GACAGGTTCACAAACAAATGTTTCTGTGACCGGGGACATGATTCATGATGCTGTTTCCCGC	1977
QY	1964	AAAAATGCGAGAGATGATCAGATTTTCAACTTTCCTTACCGACGGGACGAGAAC	2023

Db	1978	AAAACTGCGAGAAATGAATCAGAAATTTCAACATTTGCTTCAACACGGGGCTAGAGAC	2037
Oy	2024	TGTTTCAGAAATCTTTCCCGCGGTCTCAGAAATCTCAACCGGTCTCAAAAAGAGACGTAT	2083
Db	2038	TGTTTAAAGTGTTCCTCCCGGGTGTCAAGAAATCTCAACCGGTCTCAAAAABAACGTAT	2097
Oy	2084	CGAAACTCTGTGCAATTCATCATCTGCTGGGGCGGGCTCCGAGATTGCTTCTCGGC	2143
Db	2098	CGAAACTCTGCGCGAATTCATCATCTGCTGGGGCGGGCGCCGAGATTGCTTCTCGGC	2157
Oy	2144	TGCGATCTGTGCAACGTGGAATCTGGAGACGTGTCTTTCTAGCAATTAATTAAC	2203
Db	2158	TGCGAATCTGTGCAACGTGGAACCTGGAGACGTGTCTTTCTAGCAATTAATTAAC	2217
Oy	2204	AGGTATGAGCTGCCATGGTTATCTTTCAGATTTGCTCTGAGGACAACTCTCTGAGGCAT	2263
Db	2218	AGGTATGAGCTGCCATGGTTATCTTTCAGATTTGCTCTGAGGACAACTCTCTGAGGCAT	2277
Oy	2264	TCGGCAGTGTGGGACTTGAACCTTGAAGCCCGAAACCCAAAGCCAAACGCAAAAACA	2323
Db	2278	TGGGAGTGGTGGGACCTGAACCTTGAAGCCCGAAACCCAAAGCCAAACGCAAAAACA	2337
Oy	2324	GGACGAGCGCGGGGTCTGTGCTTCTGTGCTTCAAGTAACTCTCGAACCTTCAACGCACT	2383
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Db	2938	AGTCATTAACCAACCAAGCACCCCGAACAATGGGCTTGGCCCACTTAACAACAACCTCTCAAA	2997
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 VERSION AX753250.1 GI:32166107
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 SOURCE
 ORGANISM
 Adeno-associated virus 9
 Adeno-associated virus 9
 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
 unclassified Dependovirus.
 REFERENCE
 1
 Gao, G., Wilson, J.M. and Alvira, M.
 A method of detecting and/or identifying adeno-associated virus
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 Patent: EP 1310571-A 5 14-MAY-2003;
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 Db 123 GCTTTGGCAATTTTGGCAACCAAGTGTCAATTTGAAGGTATTAATGAGTGA 182

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OY	335	GAGATTGTGATTTAAGGTCGCCAGCACTTTGACGAGCATCTGCCGGCATTTTCTGACAGC	394
Db	243	GAGATTGTGATCAAGGTGCCAGGCACTTGGACGAGCACCTGCCGGCATTTTCTGACTCT	302
OY	395	TTTGTGAACCTGGGTGGCCGAGAAGGATGGGAGTTTCCGCCAGATTCTGACATGATCTTG	454
Db	303	TTTGTGAACCTGGGTGGCCGAGAAGGATGGGAGTCTGCCGCCGATTCTGACATGATCTCG	362
OY	455	AATCGATTGAGCAGGCAACCCCTGACCGTGGCGGAGAGCTGACAGCGGACCTTCTCGTGC	514
Db	363	AATCGATTGAGCAGGCAACCCCTGACCGTGGCGGAGAGCTGACAGCGGACCTTCTCGTGC	422
OY	515	CATTGGCCCGCGGTGATTAAGGCCCGAGAGGCCCTTTCTTTGTTCAGTTTCAGAGAAGGC	574
Db	423	CAATGGCCCGCGGTGATTAAGGCCCGAGAGGCCCTTTCTTTGTTCAGTTTCAGAGAAGGC	482
OY	575	GAGTCTTACTTCCACTCTCATTTTGGTGGAGACACGGGGGTCAATTCATGGTGTCTG	634
Db	483	GAGAGCTACTTTCACCTGCACTTCTTGGTGGAGACACGGGGGTCAAGTCCATGGTGTCTA	542
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OY	695	CCGACCTCTGCCCACTGGTTGCGCGGTGACCAAGACGCGTAAATGCGCGCGAGGGGGAAAC	754
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OY	1055	GACCAAGGCTGTGATCATCTCTTAAACGCGCTCAACCTGCGCGGTCCCAAGTCAAGGCC	1114
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OY	1115	GCTCTGACCAATGCGCGAGAGTCAATGCGCTGACCAATTCGCGCCCGCATCTACTGTGTA	1174
Db	1023	GCGCTGACCAATGCGCGAGAGTCAATGCGCTGACCAATTCGCGCCCGCATCTACTGTGTA	1082
OY	1175	GGCCCCGCTCCGCCCGCGCATTTAAACCAACCGCATTTTACCGGATCTCTGAGTGAAC	1234
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OY	1235	GGCTTACGACCTTGCTTACGCGGCTCCGCTCTTTCTGCGCTGGGCCCCAAGAAAGTTTCGA	1294
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QY	1415	TTCAACGATTCGCTCGACMAAGTGTGATCTGTGTGGAGGAGGGCAAGATGACGGCCAA	1474
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QY	1475	GTCTGTGAGATCCGCCAAGGCCATTTCTCGGCGGCAGCAAGGTGCGGTGGAACCAAAATGTC	1533
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QY	1955	TTTCCCGTCAAAACATGTGAGAGATGAATAGAAATTTCAATTTGCTTACGACGAGG	2014
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QY	2075	AGGACGTATCGGAAACTCTGTGCAATTCATCTGCTGGGGCGGGCTCCCGAATGCT	2134
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Db	2043	TGCTCCGCGCTGCAATCTGTGCAAGTGTGATGCTGTGTTTCTGAGCAATTAATG	2102
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Db 4380 TC 4381
RESULT 13
CO972063
LOCUS
DEFINITION Sequence 8 from Patent WO2004108922.
ACCESSION CO972063
VERSION CO972063.1 GI:57163376

KEYWORDS
SOURCE Adeno-associated virus
ORGANISM Adeno-associated virus
Virus; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
Unclassified Dependovirus.
REFERENCE
AUTHORS Rader, D.J. and Wilson, J.M.
TITLE Methods and compositions for lowering total cholesterol levels and
treatment of heart disease
JOURNAL Patent: WO 2004/108922-A 8 16-DEC-2004;
The Trustees of The University of Pennsylvania (US)
FEATURES
source 1. .4393
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/mol_type="unassigned DNA"
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ORIGIN
Query Match 72.0%; Score 3370.4; DB 2; Length 4393;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 527; Indels 16; Gaps 9;
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OY	2069	AGAAAGAGGAGCGTATCGGAAACTCTGTGCGCAATTGATCATCTGCTGAGGGCGGGCTCCGAG	2128
Dp	1982	AGAAAGAGGAGCGTATCGGAAACTCTGTGCGCAATTGATCATCTGCTGAGGGCGGGCTCCGAG	2041
OY	2129	ATTGCTTGCTGGGCTCGGATCTGTGTCATCGTGGATCTGGATGACTGTGTGTTCTTGACGA	2188
Dp	2042	ATTGCTTGCTGGGCTCGGATCTGTGTCATCGTGGATCTGGATGACTGTGTGTTCTTGACGA	2101
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OY	2309	CAACGAGAAAGACGAGCGAGCGGCGGGGTCTGGGTGCTCTGGGCTTCAAGTACCTCGG	2368
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Dp	2342	GCACGACAGAGCTTACACACACAGAGCTGACAGCGGGGTGACAAATCCGTACTGTCGGTATTA	2401
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Db	3182	GTACGTTCTCGGCTCTGCCCAACAGGGCTGCTGCTCGTTCCGGCGAGCTGTTCAAT	3241
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Oy	3743	TGGCGTGAATTAATATCAACCTCGGCACTGCTATGCGCTCAACAAAGACGACAAAGA	3802
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RESULT 14
LOCUS CS073594 4393 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 182 from Patent WO2005033321.
ACCESSION CS073594
VERSION CS073594.1 GI:63090490
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1
AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H.
TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses thereof
JOURNAL Patent: WO 2005033321-A 182 14-APR-2005;
FEATURES The Trustees of the University of Pennsylvania (US)
source Location/Qualifiers
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ORIGIN

Query Match 72.0%; Score 3370.4; DB 2; Length 4393;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 527; Indels 16; Gaps 9;

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Db 1382 GCCAAGTGTGAGTCCGCGCAAGGCAATCTCGGCGGCAAGCAAGTGTGAGCAAC 1441
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OY	1589	ATGTGCGCGGTGATTTAGCGGGAAACAGCACCACTCTTGAGCACACAGACGCCGTTGCAGGAC	1648
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OY	1649	CGGATGTTCAATTTGAACTCAACCGCGGTCTGAGCAATGACTTTGGCAAGGTGCAAG	1708
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OY	1709	CAGGAAGTCAAGAGTCTTTCGCTGGGCGCAGGATCACTGACCCGAGGTGGCGCATGAG	1768
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OY	1769	TTTCTACGTCAAAAAGGGTGGAGCCCAACAGACCCCGCCCCGGATGAGACGGGATPAAAGC	1828
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OY	1829	GAGCCCAAGCGGGCGTGCCTCCCTCAGTGCAGATCCATCGACTGACGCGGAAAGAGCT	1888
Db	1742	GAGCCCAAGCGGGCGTGCCTCCCTCAGTGCAGATCCATCGACTGACGCGGAAAGAGACT	1801
OY	1889	CCGGTGAACCTTGGCCGACAGGTTACCAAAACAATGTTCTGTCACGCGGGCATGCTTACG	1948
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OY	1949	ATGCTGTTTCCCTGCAAAAACATGCGAGAGAAATGATCAGAATTTCAACATTTGCTTACG	2008
Db	1862	ATGCTGTTTCCCTGCAAAAACATGCGAGAAATGATCAGAATTTCAACATTTGCTTACCA	1921
OY	2009	CACGGGACCAAGACTGTGTCAGAAATGTTTTCCCGGCGGTGTCAGAAATCTCAACCGGTGTC	2068
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ACCESSION AX753249
VERSION AX753249.1 GI:32166106
KEYWORDS
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ORGANISM Adeno-associated virus - 8
Virus; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
unclassified Dependovirus.

REFERENCE
AUTHORS 1
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The Trustees of The University of Pennsylvania (US)
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Db 65 AGCGTGAAGTAAATTAAGTATAGGAGG--GAGTGTCTGTATTAAGTGTCAAGTACT 121
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	128.4	2.7	195	8	CO888893
C 3	106.6	2.3	913	14	DU710412
C 4	105.2	2.2	969	14	DU710793
C 5	102.4	2.2	917	14	DU710478
C 6	102.4	2.2	1165	14	DU710876
C 7	102.2	2.2	900	14	DU710553
C 8	101.6	2.2	835	14	DU710062
C 9	101.4	2.2	894	14	DU710660
C 10	101.2	2.2	895	14	DU709924
C 11	100.8	2.2	896	14	DU709985
C 12	100.6	2.1	919	14	DU710573
C 13	100.6	2.1	945	14	DU710776
C 14	100.4	2.1	937	14	DU710803
C 15	100.4	2.1	943	14	DU710346
C 16	100.2	2.1	920	14	DU710527
C 17	99.8	2.1	1032	14	DU710321
C 18	99.8	2.1	1051	14	DU710319
C 19	99.8	2.1	1057	14	DU710692

C 20	99.6	2.1	911	14	DU710661
C 21	99.4	2.1	882	14	DU710048
C 22	99.4	2.1	895	14	DU710511
C 23	99.4	2.1	916	14	DU710467
C 24	99.4	2.1	946	14	DU710802
C 25	99.4	2.1	961	14	DU710790
C 26	99.4	2.1	977	14	DU710516
C 27	99.4	2.1	1104	14	DU710637
C 28	99.2	2.1	958	14	DU710698
C 29	99	2.1	919	14	DU710988
C 30	99	2.1	937	14	DU710685
C 31	98.8	2.1	921	14	DU710471
C 32	98.8	2.1	938	14	DU710826
C 33	98.6	2.1	982	14	DU710448
C 34	98.6	2.1	980	14	DU710856
C 35	98.4	2.1	859	14	DU710005
C 36	98.4	2.1	859	14	DU710905
C 37	98.4	2.1	878	14	DU709966
C 38	98.4	2.1	888	14	DU710228
C 39	98.4	2.1	891	14	DU709911
C 40	98.4	2.1	898	14	DU710025
C 41	98.4	2.1	912	14	DU710452
C 42	98.4	2.1	912	14	DU710972
C 43	98.4	2.1	922	14	DU710037
C 44	98.4	2.1	922	14	DU710560
C 45	98.4	2.1	925	14	DU710832

ALIGNMENTS

RESULT 1
CO892248/264 bp mRNA linear EST 01-SEP-2004
LOCUS BO892248.20573 normal cattle brain Bos taurus cDNA clone
DEFINITION RZPDp1056M0360Q 5', mRNA sequence.
ACCESSION CO892248
VERSION CO892248.1 GI:51822548
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE Hemmig, S., Janitz, M., Herwig, R. and Williams, J.
AUTHORS Generation, annotation, evolutionary analysis and database
TITLE integration of 14969 cattle EST clusters
JOURNAL unpublished (2004)
COMMENT Contact: Hemmig S
Laboratory 123, dept. Lebrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hemmig@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (http://www.rzpd.de).

PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATCTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATACGCGACGCTGCGAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCGGAATTCCTCCGGGT-3' (M13RSP).

FEATURES

source location/Qualifiers
1..264
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="RZPDp1056M0360Q"

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/sex="female"
/tissue_type="brain tissue"
/dev_stage="adult brain"
/clone_lib="normal cattle brain"
/notes="Organ: brain; Vector: pSport1, Site_1: NotI,
Site_2: SalI; Random primed and directionally cloned in
pSport1 vector using NotI
(5'-pGACTAGTTCATGATCGGAGCGGCCGCC (T)15-3' and SalI 5'-
TCGACCCAGCGGTCGCG-3' adapters (Gibco BRL) "
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ORIGIN

```
Query Match 4.0%; Score 187.2; DB 8; Length 264;
Best Local Similarity 81.8%; Pred. No. 6.8e-39;
Matches 216; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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OY 4054 GTCCATTTGGGCGCAAAATTCCTCACAGSAGACATTTCAACCCGCTCCTCATAGG 4113
DB 264 GTCCATTTGGGCGCAATTCACACTCGAGCAGCATTTTCACCCCTCCTCATAGG 205
OY 4114 GCGGCTTGGACTTAAGACCCGCTCCTCATGATCCTCATCAAAAACAGCGCTGTTCTG 4173
DB 204 GGGGATTTGGACTTAATACCTCCTCCACAGATTTTATCAAGAACAGCGGTTCTG 145
OY 4174 CGAATCTCCGCGCAGAGTTTTCGCTACAAAGTTTCTTCATTCATCAACCGATTTTCA 4233
DB 144 CGAGTCTTCGAGCAGCTTCAGTGGCGCAAGTTTGTTCATTCACACAGTACTCCA 85
OY 4234 CAGGACAGTGAAGCGGTGAATGGAATGGGAGCTGCAGAAAAGAACGCAAGCTTGA 4293
DB 84 CGGTCAGGTGACGCTGAGATTTGAGTGGAGCTGGGAGAGAAAGCAAGCAAGCTTGA 25
OY 4294 ATCCGAAGTGCAGTATACATCTA 4317
DB 24 ATCCGAATTCAGTACATCTCA 1
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RESULT 2
LOCUS CO888893 195 bp mRNA linear EST 01-SEP-2004
DEFINITION Bovgen.17218 normal cattle brain Bos taurus cDNA clone
ACCESSION CO888893
VERSION CO888893.1 GI:51819178
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
TITLE Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 195)
Hennig,S., Janitz,M., Herwig,R. and Williams,J.
Generation, annotation, evolutionary analysis and database
integration of 14969 cattle EST clusters
Unpublished (2004)
```

JOURNAL

```
COMMENT Contact: Hennig S
Laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
The library was characterized by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones that display the same hybridisation matrix with a
battery of 200 emer oligonucleotides are grouped into clusters. One
clone per ONFP cluster was selected for sequencing. cDNA clones and
filters are distributed via Deutsches Ressourcenzentrum fuer
Genomforschung GmbH (http://www.rzpd.de) .
```

```
PCR primers
FORWARD: 5' CCCGAGGCTTACACTTATGCTTCGGCTCG 3' (M13SP) 5'-seq
BACKWARD: 5' GCTATTACGCAAGCTGGCAAGGGGATG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGATCCGGAATTCGGGCT-3' (M13RSP).
```

FEATURES

Location/Qualifiers

source

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1. 195
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="RZPDp10560960Q"
/sex="female"
/tissue_type="brain tissue"
/dev_stage="adult brain"
/clone_lib="normal cattle brain"
/notes="Organ: brain; Vector: pSport1, Site_1: NotI,
Site_2: SalI; Random primed and directionally cloned in
pSport1 vector using NotI
(5'-pGACTAGTTCATGATCGGAGCGGCCGCC (T)15-3' and SalI 5'-
TCGACCCAGCGGTCGCG-3' adapters (Gibco BRL) "
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ORIGIN

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Query Match 2.7%; Score 128.4; DB 8; Length 195;
Best Local Similarity 78.9%; Pred. No. 5.9e-23;
Matches 153; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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OY 4224 CAGTATTCACAGGACAGTGAAGGAGATTTGAATGGAGGCTGCAGAAAGAACAGC 4283
DB 194 CAGTATTCACAGGACAGTGAAGGAGATTTGAATGGAGGCTGCAGAAAGTAAACAGC 135
OY 4284 AAACGCTGAATCCCGAAGTGCATATATCACTATATCAAAATCTGCCAAGTTGAT 4343
DB 134 AAACGCTGAATCCCGAATTCAGTACATTCACATCAACAAGTCTGTTAATGTGAT 75
OY 4344 TTCAGTGTGACAAATTCGATTTATCTGAGGCTGCCCCATTTGGCACCCTTACTTC 4403
DB 74 TTTATATGTGACATTAATGAGCTGTATTCAGAGCTTGCCTCCCATTTGGCACCAATACCTG 15
OY 4404 ACCGTCCTCCCTGTA 4417
DB 14 ACTGTATATGTGTA 1
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```
RESULT 3
LOCUS DU710412 913 bp DNA linear GSS 15-NOV-2005
DEFINITION aav01.fpol0q008y1 Adeno-Associated Virus Vector Integration
survey sequence.
ACCESSION DU710412
VERSION DU710412.1 GI:82414138
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Hominidae; Homo.
1 (bases 1 to 913)
Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
Russell,D.W.
Large-scale Analysis of Adeno-Associated Virus Vector Integration
Sites
```

JOURNAL

```
COMMENT Journal of Virology 79 (17), 11434-11442 (2005)
Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSP RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
```

AAV Vector:Chromosome Junction Sequences rescued as plasmids in
bacteria. Files with names differing only by x1 or y1 contain
sequence reads from either end of the same AAV provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer was used
to initiate sequencing reactions.

FEATURES

Location/Qualifiers


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source
1. .913
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aaV01_fp010q008"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"
/clone_11b="Adeno-Associated Virus Vector Integration Junctions"
/notes="Vector: AAV2-T0A; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV vector provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions."

ORIGIN
Query Match 2.3%; Score 106.6; DB 14; Length 913;
Best Local Similarity 96.5%; Pred. No. 8e-17;
Matches 109; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 35 CTGAGCGCCGGCGACCAAGGTCGCGCCGCGCGGGGCTTTGCCGGGGGCGCTCAGCA 94
|||
Dh 170 CTTTGCTGGGGCGACCAAGGTCGCGCCGCGCGGGGCTTTGCCGGGGGCGCTCAGCA 111
|||
Oy 95 GCGAGCGAGCGCGCAGAGAGGGAGTGCGCACTCCATCAGTAGGGGTTCTGG 147
|||
Dh 110 GCGAGCGAGCGCGCAGAGAGGGAGTGCGCACTCCATCAGTAGGGGTTCTGG 58
|||

RESULT 4
DUT10793/c
LOCUS
DEFINITION
DUT10793 969 bp DNA linear GSS 15-NOV-2005
aav01_fp014q065x1 Adeno-Associated Virus Vector Integration
Junctions Homo sapiens genomic clone aav01_fp014q065, genomic
survey sequence.
DUT10793
DUT10793.1 GI:82414519
GSS.
SOURCE
Homo sapiens (human)
Organism
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 969)
Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
Russell,D.W.
Large-scale Analysis of Adeno-Associated Virus Vector Integration
Sites
Journal of Virology 79 (17), 11434-11442 (2005)
Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB RK349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in
bacteria. Files with names differing only by x1 or y1 contain
sequence reads from either end of the same AAV provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer was used
to initiate sequencing reactions.
Seq primer: right, 5'-ATCACGAGCGCCCTTCGCTTCAGG
Class: viral tagged.
Location/Qualifiers
1. .969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp014q065"

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ORIGIN	/sex="male" /cell_type="Human Primary Fibroblasts" /cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ" /clone_lib="Adeno-Associated Virus Vector Integration Junctions" /note="Vector: AAV2-10A; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV vector provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions."	
Query Match	2.2%	Score 105.2; DB 14; Length 969;
Best Local Similarity	93.2%;	Pred. No. 2e-16;
Matches	110; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
Qy	30	GCTCACTAGAGCCGGGCGAGCAAGGTCGCCCGGAGCCCGGGGCTTGGCCGGGGGCGCTC 89
Db	178	GCTTCCAAAGGTGTCGCCGACCAAGAGTGCCTCGAGCCCGGCTTTGGCCCGGGGCGCTC 119
Qy	90	AGTAGAGCAGCGAGCGCGCAGAGAGAGGAGTGGCCCACTCATCTAGAGGGTTCCTGG 147
Db	118	AGTAGCGAGCGAGCGCGCCGACAGAGGAGTGGCCCACTCATCTAGAGGGTTCCTTG 61
RESULT 5		
DU710478/c	917 bp	DNA linear GSS 15-NOV-2005
LOCUS		
DEFINITION	aav01_fp010q068y1 Adeno-Associated Virus Vector Integration Junctions Homo sapiens genomic clone aav01_fp010q068, genomic survey sequence.	
ACCESSION	DU710478	
VERSION	DU710478.1	
KEYWORDS	GSS.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	1 (bases 1 to 917) Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.	
TITLE	Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites	
JOURNAL	Journal of Virology 79 (17), 11434-11442 (2005)	
COMMENT	Contact: Miller, D.G. Department of Pediatrics University of Washington HSB R3439A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195, USA Tel: 206 685 3882 Fax: 206 221 5132 Email: dgmiller@u.washington.edu AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions Seq primer: left, 5'-GATTAAGCTGTCAACATGAGATTTC Class: viral tagged.	
FEATURES	Location/Qualifiers	
source	1..917 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="aav01_fp010q068" /sex="male" /cell_type="Human Primary Fibroblasts" /cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ" /clone_lib="Adeno-Associated Virus Vector Integration	

Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
Sequences rescued as plasmids in bacteria. Files with
names differing only by x1 or y1 contain sequence reads
from either end of the same AAV vector provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer
was used to initiate sequencing reactions."

ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 917;
Best Local Similarity 90.8%; Pred. No. 1.1e-15;
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 28 TCGCTCACTGAGCGCGCGCAAGGTGCGCCGAGCGCGGCTTTGCCGGGCGGCC 87
Db 176 TTGCTCATCTCGGGTGTGTACCAAGGTGCGCCGAGCGCGGCTTTGCCGGGCGGCC 117
Qy 88 TCAGTGAGCGAGCGAGCGCGCAGAGAGGAGTGCGCACTCCATCACTAGGGGTTCTGTG 147
Db 116 TCAGTGAGCGAGCGAGCGCGCAGAGAGGAGTGCGCACTCCATCACTAGGGGTTCTGTG 57

RESULT 6
DUT10876/c 1165 bp DNA linear GSS 15-NOV-2005
LOCUS aav01_fp017q002y1 Adeno-Associated Virus Vector Integration
DEFINITION Junctions Homo sapiens genomic clone aav01_fp017q002, genomic
survey sequence.

ACCESSION
DUT10876
VERSION
DUT10876.1 GI:82414602
KEYWORDS
GSS.

SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 1165)
Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
Russell,D.W.

TITLE
Large-scale Analysis of Adeno-Associated Virus Vector Integration
Sites
JOURNAL
Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT
Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in
bacteria. Files with names differing only by x1 or y1 contain
sequence reads from either end of the same AAV provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer was used
to initiate sequencing reactions.
Seq primer: left, 5'-GATTAAGCTGTCAACATGAGAAATTC
Class: viral tagged.

FEATURES
source
Location/Qualifiers

1..1165
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp017q002"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical
Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration
Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
Sequences rescued as plasmids in bacteria. Files with
names differing only by x1 or y1 contain sequence reads
from either end of the same AAV vector provirus. 'y1'

indicates the 'left' and 'x1' indicates the 'right' primer
was used to initiate sequencing reactions."

ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 1165;
Best Local Similarity 90.8%; Pred. No. 1.2e-15;
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 28 TCGCTCACTGAGCGCGCGCAAGGTGCGCCGAGCGCGGCTTTGCCGGGCGGCC 87
Db 226 TCACCCACTAATCTTGCTGAAGCCCAAGGTGCGCCGAGCGCGGCTTTGCCGGGCGGCC 167
Qy 88 TCAGTGAGCGAGCGAGCGCGCAGAGAGGAGTGCGCACTCCATCACTAGGGGTTCTGTG 147
Db 166 TCAGTGAGCGAGCGAGCGCGCAGAGAGGAGTGCGCACTCCATCACTAGGGGTTCTGTG 107

RESULT 7
DUT10553/c 900 bp DNA linear GSS 15-NOV-2005
LOCUS aav01_fp011q043y1 Adeno-Associated Virus Vector Integration
DEFINITION Junctions Homo sapiens genomic clone aav01_fp011q043, genomic
survey sequence.

ACCESSION
DUT10553
VERSION
DUT10553.1 GI:82414279
KEYWORDS
GSS.

SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 900)
Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
Russell,D.W.

TITLE
Large-scale Analysis of Adeno-Associated Virus Vector Integration
Sites
JOURNAL
Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT
Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in
bacteria. Files with names differing only by x1 or y1 contain
sequence reads from either end of the same AAV provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer was used
to initiate sequencing reactions.
Seq primer: left, 5'-GATTAAGCTGTCAACATGAGAAATTC
Class: viral tagged.

FEATURES
source
Location/Qualifiers

1..900
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp011q043"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical
Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration
Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
Sequences rescued as plasmids in bacteria. Files with
names differing only by x1 or y1 contain sequence reads
from either end of the same AAV vector provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer
was used to initiate sequencing reactions."

ORIGIN

Query Match 2.2%; Score 102.2; DB 14; Length 900;

QY 105 GCGGAGAGGAGGCGCAACTCCATCATAGGGGTTCTTG 147
 Db 103 GCGGAGAGGAGGAGTGGCCAACTCCATCATAGGGGTTCTTG 61
 RESULT 10
 LOCUS DU709924/c
 DEFINITION aav01_f0003q029y1 Adeno-Associated Virus Vector Integration
 SURVEY sequence.
 ACCESSION DU709924 895 bp DNA linear GSS 15-NOV-2005
 VERSION DU709924
 KEYWORDS GSS.
 SOURCE DU709924.1 GI:82413650
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 895)
 Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
 Russell,D.W.
 Large-scale Analysis of Adeno-Associated Virus Vector Integration
 Sites
 Journal of Virology 79 (17), 11434-11442 (2005)
 CONTACT: Miller, D.G.
 Department of Pediatrics
 University of Washington
 HSB R349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
 USA
 Tel: 206 685 3882
 Fax: 206 221 5132
 Email: dgmiller@u.washington.edu
 AAV Vector:Chromosome Junction Sequences rescued as plasmids in
 bacteria. Files with names differing only by x1 or y1 contain
 sequence reads from either end of the same AAV provirus. 'y1'
 indicates the 'left' and 'x1' indicates the 'right' primer was used
 to initiate sequencing reactions.
 Seq primer: left, 5'-GATTAAGCTGTCAACATGGAATTC
 Class: viral tagged.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="aav01_f0003q029"
 /sex="male"
 /cell_type="Human Primary Fibroblasts"
 /cell_line="GM05387, Coriell Institute for Medical
 Research, Camden, NJ"
 /clone_lib="Adeno-Associated Virus Vector Integration
 Junctions"
 /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
 Sequences rescued as plasmids in bacteria. Files with
 names differing only by x1 or y1 contain sequence reads
 from either end of the same AAV vector provirus. 'y1'
 indicates the 'left' and 'x1' indicates the 'right' primer
 was used to initiate sequencing reactions."
 ORIGIN
 Query Match 2.2%; Score 101.2; DB 14; Length 895;
 Best Local Similarity 93.0%; Pred. No. 2.3e-15;
 Matches 106; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 34 ACTGAGCGCGGCGCAACAAGTGCCTCCGAGCCCGGCTTGGCCGGGCGGCTCAATG 93
 Db 170 ACGGGGTCTGACAGCCAAAGTGCCTCCGAGCCCGGCTTGGCCGGGCGGCTCAATG 111
 QY 94 AGCGAGCGAGCGCGCAAGAGAGGAGTGGCCAACTCATCTAGGGGTTCTTG 147
 Db 110 AGCGAGCGAGCGCGCAAGAGAGGAGTGGCCAACTCATCTAGGGGTTCTTG 57

RESULT 11
 LOCUS DU709985/c
 DEFINITION aav01_f0003q079y1 Adeno-Associated Virus Vector Integration
 Junctions Homo sapiens genomic clone aav01_f0003q079, genomic
 survey sequence.
 ACCESSION DU709985 896 bp DNA linear GSS 15-NOV-2005
 VERSION DU709985
 KEYWORDS GSS.
 SOURCE DU709985.1 GI:82413711
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 896)
 Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
 Russell,D.W.
 Large-scale Analysis of Adeno-Associated Virus Vector Integration
 Sites
 Journal of Virology 79 (17), 11434-11442 (2005)
 CONTACT: Miller, D.G.
 Department of Pediatrics
 University of Washington
 HSB R349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
 USA
 Tel: 206 685 3882
 Fax: 206 221 5132
 Email: dgmiller@u.washington.edu
 AAV Vector:Chromosome Junction Sequences rescued as plasmids in
 bacteria. Files with names differing only by x1 or y1 contain
 sequence reads from either end of the same AAV provirus. 'y1'
 indicates the 'left' and 'x1' indicates the 'right' primer was used
 to initiate sequencing reactions.
 Seq primer: left, 5'-GATTAAGCTGTCAACATGGAATTC
 Class: viral tagged.
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="aav01_f0003q079"
 /sex="male"
 /cell_type="Human Primary Fibroblasts"
 /cell_line="GM05387, Coriell Institute for Medical
 Research, Camden, NJ"
 /clone_lib="Adeno-Associated Virus Vector Integration
 Junctions"
 /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
 Sequences rescued as plasmids in bacteria. Files with
 names differing only by x1 or y1 contain sequence reads
 from either end of the same AAV vector provirus. 'y1'
 indicates the 'left' and 'x1' indicates the 'right' primer
 was used to initiate sequencing reactions."
 ORIGIN
 Query Match 2.2%; Score 100.8; DB 14; Length 896;
 Best Local Similarity 93.8%; Pred. No. 3e-15; 7; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 36 TGAAGCCGCGCGCAACAAGTGCCTCCGAGCCCGGCTTGGCCGGGCGGCTCAATGAG 95
 Db 170 TGAAGCAAACTTCCAAAGTGCCTCCGAGCCCGGCTTGGCCGGGCGGCTCAATGAG 111
 QY 96 CGAGCGAGCGCGCAAGAGAGGAGTGGCCAACTCATCTAGGGGTTCTTG 147
 Db 110 CGAGCGAGCGCGCAAGAGAGGAGTGGCCAACTCATCTAGGGGTTCTTG 59
 RESULT 12
 LOCUS DU710573/c
 DEFINITION aav01_f0011q064x1 Adeno-Associated Virus Vector Integration

REFERENCE 1 (bases 1 to 937)
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites
JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB R3349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by xl or yl contain sequence reads from either end of the same AAV provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions.
Seq primer: right, 5'-ATCAGAGGCGCTTTCGTTCAAG
Class: viral tagged.

FEATURES
source
Location/Qualifiers
1..937
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp014q087"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by xl or yl contain sequence reads from either end of the same AAV vector provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions."

ORIGIN
Query Match 2.1%; Score 100.4; DB 14; Length 937;
Best Local Similarity 90.7%; Pred. No. 3.9e-15;
Matches 107; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 30 GCTCAGTGGCGCGGCGAGCAAGGTGCGCGCGGCTTGGCGGCGGCGCTC 89
Db 178 CGAGCTTGGGCTCGAGCGCCCAAGGTGCGCGAGCGCGGCTTGGCGGCGGCTC 119
Qy 90 AGTGAGCGAGCGCGCGCAGAGAGGAGTGGCCCACTCATCACTAGGGGTTCTGG 147
Db 118 AGTGAGCGAGCGCGCGCAGAGAGGAGTGGCCCACTCATCACTAGGGGTTCTGG 61

RESULT 15
DU710346/c 943 bp DNA linear GSS 15-NOV-2005
LOCUS aav01_fp008q066y1 Adeno-Associated Virus Vector Integration
DEFINITION Junctions Homo sapiens genomic clone aav01_fp008q066, genomic
survey sequence.
ACCESSION DU710346
VERSION DU710346.1 GI:82414072
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 943)
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites

JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB R3349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by xl or yl contain sequence reads from either end of the same AAV provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions.
Seq primer: left, 5'-GATAGCTGTCAACATGAGATTTC
Class: viral tagged.

FEATURES
source
Location/Qualifiers
1..943
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp008q066"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by xl or yl contain sequence reads from either end of the same AAV vector provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions."

ORIGIN
Query Match 2.1%; Score 100.4; DB 14; Length 943;
Best Local Similarity 99.0%; Pred. No. 3.9e-15;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 46 CGACCAAGGTGCGCGCGAGCGCGGCTTGGCGGCGGCGCTCAGTGAAGCGAGCG 105
Db 158 CGACCAAGGTGCGCGCGAGCGCGGCTTGGCGGCGGCGCTCAGTGAAGCGAGCG 99
Qy 106 CGCAGAGGAGTGGCGCAACTCATCACTAGGGGTTCTGG 147
Db 98 CGCAGAGGAGTGGCGCAACTCATCACTAGGGGTTCTGG 57

Search completed: June 14, 2006, 01:33:42
Job time : 20433 secs